STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 118105

TO: Minh-Tam Davis **Location: REM/3A24/3C18** **Art Unit: 1642** **Wednesday, March 31, 2004** **Case Serial Number: 10/089600**	**From: Paul Schulwitz** **Location: Biotech-Chem Library** **REM-1A65** **Phone: (571)272-2527** **paul.schulwitz@uspto.gov**

Search Notes

Examiner Davis,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

party date 09/09

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2527

STIC-Biotech/ChemLib 118105

From: Chan, Christina
Sent: Monday, March 29, 2004 3:05 PM
To: Davis, Minh-Tam; STIC-Biotech/ChemLib
Subject: RE: Rush search request for 10/089600

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----
From: Davis, Minh-Tam
Sent: Monday, March 29, 2004 11:49 AM
To: Chan, Christina
Subject: Rush search request for 10/089600

Please search in commercial database, issued patent files, PGPUB and interference:
SEQ ID NO:2.
Thank you.

MINH TAM DAVIS
ART UNIT 1642
ROOM 3A24, MB 3C18
272-0830

RECEIVED
MAR 29 2004
TECH CENTER 1600/2900
(STIC)

Searcher:_____
Phone:_____
Location:_____
Date Picked Up:_____
Date Completed: 3/31
Searcher Prep/Review:_____
Clerical:_____
Online time:_____

TYPE OF SEARCH:
NA Sequences:_____
AA Sequences:_____
Structures:_____
Bibliographic:_____
Litigation:_____
Full text:_____
Patent Family:_____
Other:_____

VENDOR/COST (where applic.)
STN:_____
DIALOG:_____
Questel/Orbit:_____
DRLink:_____
Lexis/Nexis:_____
Sequence Sys.:_____
WWW/Internet:_____
Other (specify):_____

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2004, 14:29:47 ; Search time 60 Seconds
(without alignments)
1492.793 Million cell updates/sec

Title: US-10-089-600-2
Perfect score: 1745
Sequence: 1 MAKNPPENCEDCHILNAEAF.....VICRVIMPCNWWVARMLGRV 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1745	100.0	317	3	AAY71262	Aay71262 Human cho
2	1745	100.0	317	3	AAY99430	Aay99430 Human PRO
3	1745	100.0	317	3	AAB25665	Aab25665 Human sec
4	1745	100.0	317	4	AAB66179	Aab66179 Protein o
5	1745	100.0	317	4	AAB96985	Aab96985 Human ang
6	1745	100.0	317	4	AAU12433	Aau12433 Human PRO
7	1745	100.0	317	4	AAB87583	Aab87583 Human PRO
8	1745	100.0	317	4	AAB99936	Aab99936 Human new
9	1745	100.0	317	4	AAB82755	Aab82755 Human cho
10	1745	100.0	317	5	ABG95908	Abg95908 Human sec
11	1745	100.0	317	6	ABO17877	Abo17877 Novel hum
12	1745	100.0	317	6	ABU81131	Abu81131 Human PRO
13	1745	100.0	317	6	ABU90933	Abu90933 Novel hum
14	1745	100.0	317	6	ABO33992	Abo33992 Human sec
15	1745	100.0	317	6	ABU72009	Abu72009 Novel hum
16	1745	100.0	317	6	ABU66831	Abu66831 Human PRO
17	1745	100.0	317	6	ABU71563	Abu71563 Human sec
18	1745	100.0	317	6	ABU59912	Abu59912 Novel sec
19	1745	100.0	317	6	ABU72344	Abu72344 Human PRO
20	1745	100.0	317	6	ABU91017	Abu91017 Human PRO
21	1745	100.0	317	6	ABO27338	Abo27338 Human sec
22	1745	100.0	317	6	ABO25102	Abo25102 Human sec
23	1745	100.0	317	6	ABU92533	Abu92533 Human sec
24	1745	100.0	317	6	ABU81203	Abu81203 Human sec
25	1745	100.0	317	6	ABO53317	Abo53317 Novel hum
26	1745	100.0	317	6	ABU67107	Abu67107 Human sec
27	1745	100.0	317	6	ABU98320	Abu98320 Novel hum
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32	1745	100.0	317	6	ADA46043	Ada46043 Novel hum
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34	1745	100.0	317	6	ADB17173	Adb17173 Human tra
35	1745	100.0	317	6	ADA19124	Ada19124 Human PRO
36	1745	100.0	317	6	ADA61747	Ada61747 Homo sapi
37	1745	100.0	317	6	ADB19532	Adb19532 Novel hum
38	1745	100.0	317	6	ADB28073	Adb28073 Human PRO
39	1745	100.0	317	6	ADA86552	Ada86552 Novel hum
40	1745	100.0	317	6	ADB16116	Adb16116 Human PRO
41	1745	100.0	317	6	ADA47902	Ada47902 Human PRO
42	1745	100.0	317	6	ABO44296	Abo44296 Human sec
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44	1745	100.0	317	6	ADA19978	Ada19978 Novel hum
45	1745	100.0	317	6	ADA67697	Ada67697 Human PRO

ALIGNMENTS

RESULT 1
AAY71262
ID AAY71262 standard; protein; 317 AA.
XX
AC AAY71262;
XX
DT 21-SEP-2000 (first entry)
XX
DE Human chondromodulin-like protein, Zchm1.
XX
KW Chondromodulin-like protein; Zchm1; human; chromosome 11p15.4; cancer;
KW cell differentiation regulator; osteoblast proliferation stimulator;
KW cytostatic; diagnostic; therapeutic; polypeptide-toxin fusion protein;
KW class II cell surface protein; transmembrane domain; gene therapy;
KW targeted cell inhibition.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 31. .50
FT /label= Transmembrane_domain
FT /note= "Alternative amino-terminal hydrophobic sequence"
FT Domain 34. .48
FT /label= Transmembrane_domain
FT /note= "Amino-terminal hydrophobic sequence"
FT Protein 48. .311
FT /note= "Mature soluble form of chondromodulin-like
FT protein, Zchm1-1"
FT Protein 202. .311
FT /note= "Mature soluble form of chondromodulin-like
FT protein, Zchm1-2"
FT Cleavage-site 213. .214
FT /label= Dibasic_cleavage_site
FT /note= "Alternative cleavage site as stated in page 13 of
FT the specification"
FT Cleavage-site 214. .215
FT /note= "Conserved site of cleavage that produces mature
FT Zchm1 protein"
FT Protein 215. .317
FT /note= "Mature chondromodulin-like protein, Zchm1-1"
FT Protein 255. .317
FT /note= "Mature chondromodulin-like protein, Zchm1-2"
FT Domain 255. .316
FT /label= Carboxyl_terminal_domain
FT /note= "Has sequence identity to bovine and human
FT chondromodulin-I (Chm-I)"
XX
PN WO200029579-A1.

XX
PD 25-MAY-2000.
XX
PF 12-NOV-1999; 99WO-US026909.
XX
PR 13-NOV-1998; 98US-00191986.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Lok S, Presnell SR;
XX
DR WPI; 2000-387792/33.
DR N-PSDB; AAD01066.
XX
PT Polynucleotide encoding mammalian chondromodulin-like polypeptide useful
PT for gene therapy of various disorders by regulating growth or
PT differentiation of cells especially cancer cells.
XX
PS Claim 2; Page 77-78; 87pp; English.
XX
CC The present sequence is the human chondromodulin-like protein, Zchm1. The
CC presence of an amino-terminal hydrophobic transmembrane domain, is a
CC structural feature of class II cell surface proteins. Zchm1 may be
CC anchored on the cell membrane, via its transmembrane domain. It has
CC sequence homology to bovine and human Chm-I. The Zchm1 locus is mapped to
CC chromosome 11p15.4. It functions as a cell differentiation regulator and
CC osteoblast proliferation stimulator. Zchm1 can be used as growth or
CC differentiation regulator for cells, especially the mesenchymal,
CC myogenic, chondrogenic or endothelial cells. Zchm1 proteins or antibodies
CC are useful for identifying or treating tissues or organs expressing the
CC anti-complementary molecule, e.g., receptor or antigen. The Zchm1
CC polypeptides conjugated to drugs, toxins, radionuclides are useful for in
CC vivo diagnostic or therapeutic applications and polypeptide-toxin fusion
CC proteins are useful for targeted cell or tissue inhibition or ablation
CC for treating various disorders, especially cancer. It is useful for gene
CC therapy of disorders associated with altered Zchm1 activity
XX
SQ Sequence 317 AA;

Query Match 100.0%; Score 1745; DB 3; Length 317;
Best Local Similarity 100.0%; Pred. No. 6.6e-153;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
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Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
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Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317
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RESULT 2
AAY99430
ID AAY99430 standard; protein; 317 AA.
XX
AC AAY99430;
XX
DT 08-AUG-2000 (first entry)
XX
DE Human PRO1565 (UNQ771) amino acid sequence SEQ ID NO:322.
XX
KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX
OS Homo sapiens.
XX
PN WO200012708-A2.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US020111.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
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PR 16-SEP-1998; 98US-0100584P.
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PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
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PR 24-SEP-1998; 98US-0101915P.
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PR 29-SEP-1998; 98US-0102330P.
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PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
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PR 06-OCT-1998; 98US-0103258P.
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PR 08-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
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PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
XX
DR WPI; 2000-237871/20.
DR N-PSDB; AAA37112.
XX
PT New mammalian DNA sequences encoding transmembrane, receptor or secreted
PT PRO polypeptides, useful for screening of potential peptide or small
PT molecule inhibitors of the relevant receptor/ligand interactions.
XX
PS Claim 12; Fig 182; 773pp; English.
XX
CC AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
CC transmembrane and receptor PRO proteins can be used for screening of
CC potential peptide or small molecule inhibitors of the relevant
CC receptor/ligand interactions. The polypeptides and nucleotide sequences
CC encoding then have various industrial applications, including uses as
CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
CC primers and hybridisation probes used in the isolation of the PRO
CC polypeptides from the present invention
XX
SQ Sequence 317 AA;

Query Match 100.0%; Score 1745; DB 3; Length 317;
Best Local Similarity 100.0%; Pred. No. 6.6e-153;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317
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RESULT 3
AAB25665
ID AAB25665 standard; protein; 317 AA.
XX
AC AAB25665;
XX
DT 04-DEC-2000 (first entry)
XX
DE Human secreted protein sequence encoded by gene 1 SEQ ID NO:54.
XX
KW Human; secreted protein; immunosuppressive; immunostimulant; nootropic;
KW antiinflammatory; cardiant; vulnerary; antiulcer; anticonvulsant;
KW antiparkinsonian; neuroprotective; antiviral; antibacterial; cytostatic;
KW antiparasitic; thrombolytic; anticoagulant; antiarteriosclerotic;
KW gene therapy; vaccine; chemotaxis-modulator; angiogenesis-modulator;
KW cancer; immune system disorder; hyperproliferative disorder; infection;
KW cardiovascular disorder; neurological disease; wound healing.
XX
OS Homo sapiens.
XX
PN WO200043495-A2.
XX
PD 27-JUL-2000.
XX
PF 18-JAN-2000; 2000WO-US000903.
XX

PR 19-JAN-1999; 99US-0116330P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Ebner R, Young PE, Ni J, Moore PA;
PI Komatsoulis G, Birse CE;
XX
DR WPI; 2000-499225/44.
DR N-PSDB; AAA87666.
XX
PT New isolated polynucleotide encoding a secreted protein useful for
PT preventing, treating or ameliorating a medical condition.
XX
PS Claim 11; Fig 1A-B; 451pp; English.
XX
CC The polynucleotide sequences given in AAA87666 to AAA87708 encodes the
CC human secreted proteins given in AAB25665 to AAB25755. Human secreted
CC proteins have activities based on the tissues and cells the genes are
CC expressed in. Examples of activities include: immunosuppressive;
CC immunostimulant; antiinflammatory; cardiant; vulnerary; antiulcer;
CC nootropic; antiviral; anticonvulsant; antiparkinsonian; neuroprotective;
CC antibacterial; antiparasitic; thrombolytic; anticoagulant;
CC antiarteriosclerotic and cytostatic. The secreted proteins and their
CC polynucleotides can be used in gene therapy and as vaccines, chemotaxis-
CC modulators and angiogenesis- modulators. The human secreted proteins and
CC polynucleotides can be used for diagnosing (the susceptibility to) a
CC pathological condition by determining the presence or absence of a
CC mutation in the polynucleotide or determining the presence or amount of
CC expression of the protein. The polynucleotides and proteins can also be
CC used in the treatment and diagnosis of cancer, diseases of the immune
CC system, hyperproliferative disorders, cardiovascular disorders and
CC neurological disease. They can also be used to promote wound healing and
CC to fight infection. AAA87657 to AAA87665 and AAB25664 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 317 AA;

Query Match 100.0%; Score 1745; DB 3; Length 317;
Best Local Similarity 100.0%; Pred. No. 6.6e-153;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317
```

RESULT 4
AAB66179
ID AAB66179 standard; protein; 317 AA.
XX
AC AAB66179;
XX
DT 02-APR-2001 (first entry)
XX
DE Protein of the invention #91.
XX
KW Secreted; transmembrane; gene therapy.
XX
OS Unidentified.
XX
PN WO200078961-A1.
XX
PD 28-DEC-2000.
XX
PF 18-FEB-2000; 2000WO-US004342.
XX
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
DR WPI; 2001-071395/08.
XX
PT Secreted and transmembrane proteins and nucleic acids designated PRO,
PT useful as hybridization probes, in chromosome and gene mapping and gene
PT therapy.
XX
PS Claim 1; Fig 182; 787pp; English.
XX
CC The present invention relates to secreted and transmembrane proteins.
CC These proteins and the DNA encoding them may be used as hybridization
CC probes, in chromosome and gene mapping and in the generation of anti-
CC sense RNA and DNA. They may also be used used to generate either
CC transgenic animals or knockout animals which are in turn useful for
CC development and screening of therapeutically useful reagents. The nucleic
CC acids may also be used in gene therapy
XX
SQ Sequence 317 AA;

Query Match 100.0%; Score 1745; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 6.6e-153;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
```

```
Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317
```

RESULT 5
AAB96985
ID AAB96985 standard; protein; 317 AA.
XX
AC AAB96985;
XX
DT 27-JUL-2001 (first entry)
XX
DE Human angiogenesis inhibitor related protein SEQ ID NO: 2.
XX
KW Human; mouse; rat; angiogenesis inhibitor; cartilage; Basedow's disease;
KW diabetic retinopathy; muscular dystrophy; chronic hepatic deficiency;
KW stomach cancer; chronic bronchitis; osteoarthritis;
KW chronic rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN WO200123557-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006804.
XX
PR 29-SEP-1999; 99JP-00275947.
XX
PA (TEIJ) TEIJIN LTD.
XX
PI Yamana K, Takahashi Y, Wada H, Kasahara Y;
XX
DR WPI; 2001-266155/27.
DR N-PSDB; AAF89155.
XX
PT Human, rat and mouse genes encoding angiogenesis inhibitors and cartilage
PT cell differentiating agents.
XX
PS Claim 1; Page 57-58; 84pp; Japanese.
XX
CC The present invention provides the protein and coding sequences of human,
CC rat and mouse angiogenesis inhibitors. These control the proliferation
CC and differentiation of cartilage calls and inhibit angiogenesis. They
CC have potential uses in the treatment of diabetic retinopathy, muscular
CC dystrophy, Basedow's disease, chronic hepatic deficiency, stomach cancer,
CC chronic bronchitis, osteoarthritis and chronic rheumatoid arthritis. The
CC present sequence is a protein given in the exemplification of the
CC invention
XX
SQ Sequence 317 AA;

```
  Query Match             100.0%;  Score 1745;  DB 4;  Length 317;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-153;
  Matches  317;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317
```

RESULT 6
AAU12433
ID AAU12433 standard; protein; 317 AA.
XX
AC AAU12433;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human PRO1565 polypeptide sequence.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIA; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US032678.
XX
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
XX
PA (GETH) GENENTECH INC.

```
XX
PI   Baker KP,  Beresini M,  Deforge L,  Desnoyers L,  Filvaroff E,  Gao W;
PI   Gerritsen ME,  Goddard A,  Godowski PJ,  Gurney AL,  Sherwood S;
PI   Smith V,  Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2001-408281/43.
DR   N-PSDB; AAS21505.
XX
PT   Isolated , secretory and transmembrane PRO polypeptide used to detect
PT   other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT   polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT   breast, prostate, cervical.
XX
PS   Claim 12; Fig 524; 813pp; English.
XX
CC   AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC   polypeptides. The PRO polypeptides are useful to detect other PRO
CC   polypeptides, to link bioactive molecules to cells expressing PRO
CC   polypeptides, to modulate biological activities of cells expressing PRO
CC   polypeptides, and to detect the presence of mammalian lung, colon,
CC   breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC   polypeptide expression in a cell sample to that in a control sample. Some
CC   of the 275 sequences are also useful to stimulate the release of tumour
CC   necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC   differentiation of chondrocytes, the proliferation or gene expression in
CC   pericyte cells, the release of proteoglycans from cartilage, the
CC   proliferation of inner ear utricular supporting cells or of T-
CC   lymphocytes, the release of a cytokine from peripheral blood monocytes
CC   (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC   polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC   muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC   VIIA. The PRO polypeptides can be used in assays to identify molecules
CC   involved in binding interactions. The polynucleotides encoding PRO
CC   polypeptides can be used to generate probes, antisense RNA/DNA,
CC   transgenic or knock out animals and can be used in gene therapy
XX
SQ   Sequence 317 AA;

  Query Match             100.0%;  Score 1745;  DB 4;  Length 317;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-153;
  Matches  317;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317


RESULT 7
AAB87583
ID   AAB87583 standard; protein; 317 AA.
XX
AC   AAB87583;
XX
DT   15-MAY-2001  (first entry)
XX
DE   Human PRO1565.
XX
KW   Human; PRO protein; mapping.
XX
OS   Homo sapiens.
XX
PN   WO200116318-A2.
XX
PD   08-MAR-2001.
XX
PF   24-AUG-2000; 2000WO-US023328.
XX
PR   01-SEP-1999;   99WO-US020111.
PR   15-SEP-1999;   99WO-US021090.
PR   07-DEC-1999;   99US-0169495P.
PR   09-DEC-1999;   99US-0170262P.
PR   11-JAN-2000; 2000US-0175481P.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   01-MAR-2000; 2000WO-US005601.
PR   03-MAR-2000; 2000US-0187202P.
PR   21-MAR-2000; 2000US-0191007P.
PR   30-MAR-2000; 2000WO-US008439.
PR   25-APR-2000; 2000US-0199397P.
PR   22-MAY-2000; 2000WO-US014042.
PR   05-JUN-2000; 2000US-0209832P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi CJ,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2001-183260/18.
DR   N-PSDB; AAF92115.
XX
PT   Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT   biology, including use as hybridization probes, and in chromosome and
PT   gene mapping.
XX
PS   Claim 12; Fig 116; 278pp; English.
XX
CC   The present sequence is a human PRO polypeptide (secreted and
CC   transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC   anti-PRO antibodies are useful for preparation of a medicament useful in
CC   the treatment of a condition which is responsive to the PRO protein,
CC   agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC   employed as molecular weight markers for protein electrophoresis. The PRO
CC   coding sequence has applications in molecular biology, including use as
CC   hybridisation probes, and in chromosome and gene mapping
XX
SQ   Sequence 317 AA;

  Query Match             100.0%;  Score 1745;  DB 4;  Length 317;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-153;
  Matches  317;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317


RESULT 8
AAB99936
ID   AAB99936 standard; protein; 317 AA.
XX
AC   AAB99936;
XX
DT   27-SEP-2001  (first entry)
XX
DE   Human new chondromodulin-I (NCHM) protein SEQ ID NO:1.
XX
KW   Human; new chondromodulin-I; NCHM; CHM-I; bone; cartilage; joint; cancer;
KW   malignant tumour; pathologic angiogenesis; organ insufficiency;
KW   digestive tract failure; exocrine secretion failure; osteopathic;
KW   cytostatic; cardiovascular; gastrointestinal; abnormal vascularisation;
KW   foetal growth disorder; organ failure; digestive disorder;
KW   secretory disorder.
XX
OS   Homo sapiens.
XX
PN   WO200148203-A1.
XX
PD   05-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-JP009236.
XX
PR   27-DEC-1999;   99JP-00369946.
PR   17-FEB-2000; 2000JP-00045124.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Itoh Y,  Nishi K;
XX
DR   WPI; 2001-425668/45.
DR   N-PSDB; AAH44410, AAH44417.
XX
PT   New proteins for treating bone, cartilage and joint diseases, cancer,
PT   abnormal vascularization, fetal growth disorders, organ failure,
PT   digestive disorders and secretory disorders.
XX
PS   Claim 1; Page 69-71; 83pp; Japanese.
XX
CC   The present sequence represents the human new chondromodulin-I (NCHM)
CC   protein. NCHM has osteopathic, cytostatic, cardiovascular and
CC   gastrointestinal activities. The NCHM protein can be used for the
CC   treatment and prevention of bone, cartilage and joint diseases, cancer,
CC   abnormal vascularisation, foetal growth disorders, organ failure,
CC   digestive disorders and secretory disorders
XX
SQ   Sequence 317 AA;

  Query Match             100.0%;  Score 1745;  DB 4;  Length 317;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-153;
  Matches  317;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317


RESULT 9
AAB82755
ID   AAB82755 standard; protein; 317 AA.
XX
AC   AAB82755;
XX
DT   29-OCT-2001  (first entry)
XX
DE   Human chondromodulin-I related peptide.
XX
KW   Chondromodulin-I related peptide; ChMIrp; human; tendon; muscle;
KW   cartilage; bone; tendinitis; cachexia; muscular dystrophy; inflammation;
KW   allergy; wound healing; arthritis; infertility; vulnerary;
KW   antiinflammatory; antiallergic; antiarthritic; osteogenic; diagnosis;
KW   therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 276
FT                   /note= "Cys-276 may be replaced by Ser or Ala in a ChMIrp
FT                   polypeptide of Claim 17"
FT   Misc-difference 280
FT                   /note= "Cys-280 may be replaced by Ser or Ala in a ChMIrp
FT                   polypeptide of Claim 18"
FT   Misc-difference 281
FT                   /note= "Glu-281 may be replaced by Asp in a ChMIrp
FT                   polypeptide of Claim 19"
FT   Misc-difference 285
FT                   /note= "Gly-285 may be replaced by Pro or Ala in a ChMIrp
FT                   polypeptide of Claim 20"
FT   Misc-difference 297
FT                   /note= "Arg-297 may be replaced by Lys, Gln or Asn in a
FT                   ChMIrp polypeptide of Claim 21"
FT   Misc-difference 300
FT                   /note= "Cys-300 may be replaced by Ser or Ala in a ChMIrp
FT                   polypeptide of Claim 22"
FT   Misc-difference 306
FT                   /note= "Cys-306 may be replaced by Ser or Ala in a ChMIrp
FT                   polypeptide of Claim 23"
FT   Misc-difference 310
FT                   /note= "Val-310 may be replaced by Ile, Met, Leu, Phe,
FT                   Ala or Nle in a ChMIrp polypeptide of Claim 24"
XX
PN   WO200153344-A2.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US001700.
XX
PR   19-JAN-2000; 2000US-0176898P.
PR   28-NOV-2000; 2000US-00724310.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Nguyen H,  Jung J,  Clarkin K;
```

XX
DR WPI; 2001-536401/59.
DR N-PSDB; AAH26446, AAH26448.
XX
PT New chondromodulin-I like polypeptides and polynucleotides useful for
PT treating, preventing or ameliorating diseases resulting from abnormal
PT levels of ChMIrp, or for inducing cartilage formation and bone growth.
XX
PS Claim 14; Fig 2; 189pp; English.
XX
CC The present sequence is that of human chondromodulin-I related peptide
CC (ChMIrp), as predicted from the open reading frame of an isolated cDNA
CC clone (see AAH26446). The protein is structurally related to
CC chondromodulin-I. It is expressed in the tendons, skeletal muscle,
CC thymus, ovary, cerebral cortex, intestine M cells and in cells adjacent
CC to the hair follicle. The invention provides ChMIrp polypeptides
CC (including those having the present sequence, or at least 1 conservative
CC amino acid substitution, an insertion or deletion, or C- and/or N-
CC terminal truncation, while maintaining activity) and polynucleotides, as
CC well as vectors, host cells, antibodies and recombinant methods for
CC producing the polypeptide. It also discloses therapeutic and diagnostic
CC uses for these and related products. ChMIrp may play a role in cartilage
CC development and blood vessel formation, in the development of tendons and
CC muscle and in attachment of muscle to bone, in immune function, and as a
CC growth factor in the growth and development of various tissues. It may be
CC useful for the diagnosis and/or treatment of tendon diseases (e.g.
CC tendinitis and tendon tear), skeletal muscle diseases (e.g. cachexia and
CC muscular dystrophy), immune system dysfunction diseases (e.g.
CC inflammation, allergy, poor wound healing and arthritis) and infertility
CC diseases
XX
SQ Sequence 317 AA;

Query Match 100.0%; Score 1745; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 6.6e-153;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317
```

RESULT 10
ABG95908
ID ABG95908 standard; protein; 317 AA.
XX
AC ABG95908;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human secreted/transmembrane protein PRO1565.
XX
KW Human; secreted protein; transmembrane protein; antirheumatic;
KW antiarthritic; osteopathic; sports-related joint problem;
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN US2002119130-A1.
XX
PD 29-AUG-2002.
XX
PF 06-DEC-2001; 2001US-00006867.
XX
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0064215P.
PR 22-APR-1998; 98US-0082797P.
PR 29-APR-1998; 98US-0083495P.
PR 15-MAY-1998; 98US-0085579P.
PR 02-JUN-1998; 98US-0087759P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 11-JUN-1998; 98US-0088863P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089653P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 24-JUN-1998; 98US-0090444P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 02-JUL-1998; 98US-0091628P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097979P.
PR 01-SEP-1998; 98US-0098749P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100930P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101475P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101916P.
PR 30-SEP-1998; 98US-0102570P.
PR 06-OCT-1998; 98US-0103449P.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021194.
PR 22-DEC-1999; 99WO-US030720.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.

PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032378.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2002-731348/79.
DR N-PSDB; ABS74435.
XX
PT New isolated secreted and transmembrane PRO polypeptide useful for
PT modulating biological activity of a cell, or for treating sports-related
PT joint problems, osteoarthritis or rheumatoid arthritis.
XX
PS Claim 20; Fig 116; 399pp; English.
XX
CC The invention relates to an isolated secreted and transmembrane PRO
CC polypeptide having 80 % sequence identity to a sequence appearing as
CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
CC extracellular domain of the proteins with their associated signal peptide
CC or lacking its associated signal peptide. Also included are the nucleic
CC acids encoding the proteins, vectors, host cells, fusion proteins and
CC antibodies which specifically bind to the proteins. The proteins are
CC useful for detecting a polypeptide designated as A, B, C or D in a sample
CC suspected of containing an A, B, C or D polypeptide, by contacting the
CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
CC conjugate in the sample, where the formation of the conjugate is
CC indicative of the presence of an A, B, C or D polypeptide in the sample,
CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
CC H or I polypeptide is labeled with a detectable label or is attached to a
CC solid support. The proteins are useful for linking a bioactive molecule
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC or I, or antibodies against them are useful for modulating a biological
CC activity of a cell expressing a polypeptide designated as A, B, C or D or
CC E, F, G, H, or I. The cell is killed. The proteins are useful for
CC identifying agonists or antagonists, for the preparation of a medicament
CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic useful reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence represents a novel secreted or transmembrane protein of the
CC invention
XX
SQ Sequence 317 AA;

Query Match 100.0%; Score 1745; DB 5; Length 317;
Best Local Similarity 100.0%; Pred. No. 6.6e-153;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
Db    1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy   61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
Db   61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy  121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
Db  121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy  181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
Db  181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy  241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
Db  241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy  301 RVIMPCNWWVARMLGRV 317
Db  301 RVIMPCNWWVARMLGRV 317
```

RESULT 11
ABO17877
ID ABO17877 standard; protein; 317 AA.
XX
AC ABO17877;
XX
DT 26-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1565.
XX
KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW TNF-alpha release; cell proliferation; cell differentiation;
KW gene expression modulator; proteoglycan release; cytokine release;
KW tumour; inflammatory disease; organ failure; atherosclerosis;
KW cardiac injury; infertility; birth defect; premature aging; AIDS;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW bioreactor; tissue typing.
XX
OS Homo sapiens.
XX
PN US2003032156-A1.
XX
PD 13-FEB-2003.
XX
PF 06-MAY-2002; 2002US-00140474.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.

PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-341980/32.
DR N-PSDB; ACD24114.
XX
PT New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, axquired immunodeficiency
PT syndrome (AIDS), or cancer.
XX
PS Claim 12; Fig 524; 660pp; English.
XX
CC The invention describes an isolated nucleic acid (I) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (I) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 317 AA;

Query Match 100.0%; Score 1745; DB 6; Length 317;
Best Local Similarity 100.0%; Pred. No. 6.6e-153;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
Db 1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy 61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
Db 61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy 121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
Db 121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy 181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
Db 181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

```
Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317


RESULT 12
ABU81131
ID   ABU81131 standard; protein; 317 AA.
XX
AC   ABU81131;
XX
DT   23-JUN-2003  (first entry)
XX
DE   Human PRO polypeptide #262.
XX
KW   Human; PRO polypeptide; secreted and transmembrane protein;
KW   anti-PRO antibody; diagnostic assay; gene expression; diabetes;
KW   bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
KW   sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;
KW   hearing loss; coagulation disorder; stroke; heart attack; cardiant;
KW   antidiabetic; anorectic; vulnerary; antiarthritic; osteopathic;
KW   antirheumatic; auditory; cerebroprotective; angiogenic.
XX
OS   Homo sapiens.
XX
PN   US2003004311-A1.
XX
PD   02-JAN-2003.
XX
PF   19-DEC-2001; 2001US-00028072.
XX
PR   18-JUN-1997;   97US-0049911P.
PR   26-AUG-1997;   97US-0056974P.
PR   17-SEP-1997;   97US-0059113P.
PR   17-SEP-1997;   97US-0059115P.
PR   17-SEP-1997;   97US-0059117P.
PR   17-SEP-1997;   97US-0059122P.
PR   17-SEP-1997;   97US-0059184P.
PR   18-SEP-1997;   97US-0059263P.
PR   19-SEP-1997;   97US-0059352P.
PR   19-SEP-1997;   97US-0059588P.
PR   24-SEP-1997;   97US-0059836P.
PR   17-OCT-1997;   97US-0062250P.
PR   17-OCT-1997;   97US-0062285P.
PR   17-OCT-1997;   97US-0062287P.
PR   17-OCT-1997;   97US-0063755P.
PR   24-OCT-1997;   97US-0062814P.
PR   24-OCT-1997;   97US-0062816P.
PR   24-OCT-1997;   97US-0063045P.
PR   24-OCT-1997;   97US-0063082P.
PR   24-OCT-1997;   97US-0063127P.
PR   27-OCT-1997;   97US-0063327P.
PR   27-OCT-1997;   97US-0063329P.
PR   28-OCT-1997;   97US-0063550P.
PR   28-OCT-1997;   97US-0063561P.
PR   29-OCT-1997;   97US-0063704P.
PR   29-OCT-1997;   97US-0063733P.
PR   29-OCT-1997;   97US-0063735P.
PR   29-OCT-1997;   97US-0063738P.
PR   03-NOV-1997;   97US-0064248P.
PR   07-NOV-1997;   97US-0064809P.
PR   12-NOV-1997;   97US-0065186P.
PR   17-NOV-1997;   97US-0065846P.
PR   21-NOV-1997;   97US-0066364P.
PR   24-NOV-1997;   97US-0066453P.
PR   24-NOV-1997;   97US-0066511P.
PR   24-NOV-1997;   97US-0066770P.
PR   11-DEC-1997;   97US-0069212P.
PR   11-DEC-1997;   97US-0069278P.
PR   11-DEC-1997;   97US-0069334P.
PR   16-DEC-1997;   97US-0069694P.
PR   23-JAN-1998;   98US-0072320P.
PR   04-FEB-1998;   98US-0073612P.
PR   09-FEB-1998;   98US-0074086P.
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PR   12-MAR-1998;   98US-0077791P.
PR   20-MAR-1998;   98US-0078910P.
PR   25-MAR-1998;   98US-0079294P.
PR   27-MAR-1998;   98US-0079663P.
PR   27-MAR-1998;   98US-0079728P.
PR   31-MAR-1998;   98US-0080165P.
PR   12-JUN-1998;   98WO-US012456.
PR   14-JUL-1998;   98WO-US014552.
PR   28-AUG-1998;   98WO-US017888.
PR   10-SEP-1998;   98WO-US018824.
PR   14-SEP-1998;   98WO-US019093.
PR   14-SEP-1998;   98WO-US019094.
PR   14-SEP-1998;   98WO-US019177.
PR   16-SEP-1998;   98WO-US019330.
PR   17-SEP-1998;   98WO-US019437.
PR   07-OCT-1998;   98WO-US021141.
PR   29-OCT-1998;   98WO-US022991.
PR   29-OCT-1998;   98WO-US022992.
PR   20-NOV-1998;   98WO-US024855.
PR   01-DEC-1998;   98WO-US025108.
PR   05-JAN-1999;   99WO-US000106.
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99WO-US005190.
PR   20-APR-1999;   99WO-US008615.
PR   14-MAY-1999;   99WO-US010733.
PR   02-JUN-1999;   99WO-US012252.
PR   01-SEP-1999;   99WO-US020111.
PR   08-SEP-1999;   99WO-US020594.
PR   13-SEP-1999;   99WO-US020944.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   05-OCT-1999;   99WO-US023089.
PR   29-NOV-1999;   99WO-US028214.
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   20-DEC-1999;   99WO-US030999.
PR   30-DEC-1999;   99WO-US031243.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005746.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Beresini M,  Deforge L,  Desnoyers L,  Filvaroff E,  Gao W;
PI   Gerritsen ME,  Goddard A,  Godowski PJ,  Gurney AL,  Sherwood S;
PI   Smith V,  Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2003-352836/33.
DR   N-PSDB; ACA67255.
XX
```

PT New isolated PRO polypeptide useful for treating diabetes, rheumatoid
PT arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
PT heart attack.
XX
PS Claim 12; Fig 524; 643pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the treatment of diabetes, bone and/or cartilage disorders
CC (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
CC hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
CC (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
CC assays for PRO, by detecting its expression in specific cells, tissues or
CC serum, and for affinity purification of PRO from recombinant cell culture
CC or natural sources. ABU80870-ABU81144 represent the human PRO
CC polypeptides of the invention. Note: The sequence data for this patent
CC was obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ Sequence 317 AA;

Query Match 100.0%; Score 1745; DB 6; Length 317;
Best Local Similarity 100.0%; Pred. No. 6.6e-153;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317
```

RESULT 13
ABU90933
ID ABU90933 standard; protein; 317 AA.
XX
AC ABU90933;
XX
DT 11-JUL-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1565.
XX
KW Human; secreted and transmembrane protein; PRO; antibody therapy;
KW pharmaceutical; diagnostic; biosensor; bioreactor.
XX
OS Homo sapiens.
XX
PN US2003018173-A1.
XX
PD 23-JAN-2003.
XX
PF 01-MAY-2002; 2002US-00063515.
XX
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-401702/38.
DR N-PSDB; ACA91221.
XX
PT New antibody useful for identifying PRO polypeptides, for affinity
PT purification of PRO polypeptides, and for preparing a medicament for
PT diagnosing or treating conditions responsive to the antibody or PRO
PT polypeptide.
XX
PS Disclosure; Fig 116; 345pp; English.
XX
CC The invention describes an antibody that specifically binds to a PRO
CC polypeptide having a fully defined amino acid sequence given in the
CC specification. The antibody is useful in identifying PRO polypeptides
CC useful for various industrial applications, including pharmaceuticals,
CC diagnostics, biosensors and bioreactors. The antibody is also used for
CC affinity purification of PRO polypeptides from recombinant cell culture
CC or natural sources. The antibody, PRO polypeptide, or its agonists or
CC antagonists, may be used for preparing a medicament for diagnosing or
CC treating a condition responsive to the antibody, PRO polypeptide, or its
CC agonists or antagonists. This is the amino acid sequence of a novel human
CC secreted and transmembrane PRO polypeptide
XX
SQ Sequence 317 AA;

Query Match 100.0%; Score 1745; DB 6; Length 317;
Best Local Similarity 100.0%; Pred. No. 6.6e-153;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
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Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317
```

RESULT 14
ABO33992
ID ABO33992 standard; protein; 317 AA.
XX
AC ABO33992;
XX
DT 18-SEP-2003 (first entry)
XX
DE Human secreted/transmembrane protein PRO1565.
XX
KW Human; secreted/transmembrane protein; PRO; tumour; cancer; cytostatic.
XX
OS Homo sapiens.

```
XX
PN   US2003009013-A1.
XX
PD   09-JAN-2003.
XX
PF   01-MAY-2002; 2002US-00063519.
XX
PR   30-DEC-1998;   98KR-00062142.
PR   08-MAR-1999;   99WO-US005028.
PR   14-MAY-1999;   99US-00311832.
PR   14-MAY-1999;   99WO-US010733.
PR   25-AUG-1999;   99US-00380137.
PR   25-AUG-1999;   99US-00380138.
PR   25-AUG-1999;   99US-00380139.
PR   25-AUG-1999;   99US-00380142.
PR   15-SEP-1999;   99US-00397342.
PR   18-OCT-1999;   99US-00403297.
PR   12-NOV-1999;   99US-00423844.
PR   30-DEC-1999;   99WO-US031274.
PR   18-FEB-2000; 2000WO-US004341.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   21-MAR-2000; 2000WO-US007532.
PR   22-MAY-2000; 2000WO-US014042.
PR   02-JUN-2000; 2000WO-US015264.
PR   22-AUG-2000; 2000US-00644848.
PR   24-AUG-2000; 2000WO-US023328.
PR   18-SEP-2000; 2000US-00664610.
PR   18-SEP-2000; 2000US-00665350.
PR   08-NOV-2000; 2000US-00709238.
PR   10-NOV-2000; 2000WO-US030873.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   22-MAR-2001; 2001US-00816744.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   30-MAY-2001; 2001US-00870574.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   29-JUN-2001; 2001US-00869599.
PR   18-JUL-2001; 2001US-00908827.
PR   06-DEC-2001; 2001US-00006867.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2003-447384/42.
DR   N-PSDB; ACD81598.
XX
PT   New isolated antibody specifically binding a PRO polypeptide, useful for
PT   the preparation of a medicament for treating disorders with the aberrant
PT   expression or activity of the PRO polypeptide, such as tumor conditions
PT   and cancer.
XX
PS   Disclosure; Fig 116; 223pp; English.
XX
CC   The invention relates to an antibody that binds to a secreted or
CC   transmembrane protein designated PRO1446 appearing as ABO33941. The
CC   protein is one of 84 PRO polypeptides which (along with their encoding
CC   nucleic acids) are disclosed in the specification. The methods and
CC   compositions of the present invention are useful for the preparation of a
CC   medicament for the treatment of disorders associated with the aberrant
CC   expression or activity of the PRO polypeptide, such as tumour conditions
CC   and cancer. They can also be used to generate transgenic or knockout
CC   animals useful in the development and screening of therapeutically useful
CC   reagents. The PRO polypeptides and encoding nucleic acids can be used as
CC   molecular weight markers for protein electrophoresis, chromosome
CC   identification and tissue typing. The antibodies may be used in various
CC   diagnostic, competitive binding and/or immunoprecipitation assays. The
CC   present sequence represents a PRO polypeptide
XX
SQ   Sequence 317 AA;

  Query Match             100.0%;  Score 1745;  DB 6;  Length 317;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-153;
  Matches  317;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
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Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
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Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317


RESULT 15
ABU72009
ID   ABU72009 standard; protein; 317 AA.
XX
AC   ABU72009;
XX
DT   11-JUN-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1565.
XX
KW   Human; secreted and transmembrane polypeptide; chromosome mapping;
KW   gene mapping; transgenic animal; knockout animal;
KW   therapeutic agent screening; chromosome identification; tissue typing;
KW   gene therapy.
XX
OS   Homo sapiens.
XX
PN   US2003018183-A1.
XX
PD   23-JAN-2003.
XX
PF   01-MAY-2002; 2002US-00063512.
XX
PR   06-DEC-2001; 2001US-00006867.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2003-330984/31.
DR   N-PSDB; ACA60420.
XX
PT   New secreted and transmembrane PRO polypeptides and nucleic acid
PT   molecules encoding the polypeptides, useful in gene therapy or preparing
PT   a medicament for treating a condition that is responsive to the PRO
PT   polypeptide or antibody.
XX
PS   Disclosure; Fig 116; 409pp; English.
XX
```

CC The invention describes novel isolated PRO polypeptides. The PRO
CC polypeptides or anti-PRO antibodies are useful in preparing a medicament
CC for treating a condition that is responsive to the PRO polypeptide or
CC antibody. The PRO nucleotide sequences may be used as hybridisation
CC probes in chromosome and gene mapping, or in generating antisense RNA and
CC DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in
CC assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knockout animals, which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification, and tissue typing. The
CC PRO polypeptides and nucleic acid molecules are also useful in gene
CC therapy, and as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. This is the amino acid sequence of a novel
CC human secreted and transmembrane PRO poypeptide
XX
SQ Sequence 317 AA;

Query Match 100.0%; Score 1745; DB 6; Length 317;
Best Local Similarity 100.0%; Pred. No. 6.6e-153;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
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Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
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Db        301 RVIMPCNWWVARMLGRV 317
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Search completed: March 30, 2004, 14:31:03
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OM protein - protein search, using sw model

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Total number of hits satisfying chosen parameters: 389414

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	516	29.6	334	1	US-08-241-465B-19	Sequence 19, Appl
3	431	24.7	296	1	US-08-241-465B-21	Sequence 21, Appl
4	254.5	14.6	120	1	US-08-047-033-2	Sequence 2, Appli
5	248	14.2	121	1	US-08-047-033-1	Sequence 1, Appli
6	105.5	6.0	304	4	US-09-107-532A-7138	Sequence 7138, Ap
7	97.5	5.6	374	1	US-08-464-148-2	Sequence 2, Appli
8	97.5	5.6	374	1	US-08-385-500-2	Sequence 2, Appli
9	97.5	5.6	374	1	US-08-846-784-2	Sequence 2, Appli
10	92	5.3	384	4	US-09-134-001C-5242	Sequence 5242, Ap
11	92	5.3	899	4	US-09-134-000C-4697	Sequence 4697, Ap
12	91	5.2	354	3	US-09-068-569-2	Sequence 2, Appli
13	90.5	5.2	1096	4	US-09-134-000C-5764	Sequence 5764, Ap
14	88.5	5.1	500	4	US-09-071-035-396	Sequence 396, App
15	88.5	5.1	1074	4	US-09-071-035-358	Sequence 358, App
16	88.5	5.1	1074	4	US-09-071-035-394	Sequence 394, App
17	88	5.0	2485	5	PCT-US94-00198-1	Sequence 1, Appli
18	87.5	5.0	1167	4	US-09-661-322A-40	Sequence 40, Appl
19	87	5.0	1018	1	US-08-072-610-2	Sequence 2, Appli
20	87	5.0	1018	2	US-08-719-822B-2	Sequence 2, Appli
21	87	5.0	1018	3	US-09-092-458-2	Sequence 2, Appli
22	86.5	5.0	341	4	US-09-328-352-7664	Sequence 7664, Ap
23	86.5	5.0	368	4	US-09-819-607-5	Sequence 5, Appli
24	86	4.9	229	1	US-08-287-959-7	Sequence 7, Appli
25	86	4.9	553	4	US-09-345-473E-33	Sequence 33, Appl
26	86	4.9	2020	1	US-07-551-531-2	Sequence 2, Appli
27	86	4.9	2818	1	US-08-510-284-1	Sequence 1, Appli
28	86	4.9	2818	1	US-08-411-389-2	Sequence 2, Appli
29	86	4.9	2818	2	US-08-449-933-2	Sequence 2, Appli
30	86	4.9	2818	3	US-07-966-049A-2	Sequence 2, Appli
31	85.5	4.9	728	4	US-09-298-924-2	Sequence 2, Appli
32	85.5	4.9	1168	1	US-08-291-368-4	Sequence 4, Appli
33	85.5	4.9	1168	2	US-08-962-190-4	Sequence 4, Appli
34	85.5	4.9	1168	5	PCT-US95-10310-4	Sequence 4, Appli
35	85	4.9	624	4	US-09-512-563C-4	Sequence 4, Appli
36	85	4.9	854	2	US-08-928-692-17	Sequence 17, Appl
37	85	4.9	854	4	US-09-339-972-17	Sequence 17, Appl
38	85	4.9	2485	5	PCT-US94-00198-2	Sequence 2, Appli
39	84.5	4.8	369	4	US-09-819-607-2	Sequence 2, Appli
40	84.5	4.8	384	4	US-09-801-876B-6	Sequence 6, Appli
41	84.5	4.8	384	4	US-10-254-869-6	Sequence 6, Appli
42	84.5	4.8	399	4	US-09-819-607-4	Sequence 4, Appli
43	84.5	4.8	419	4	US-09-799-875-14	Sequence 14, Appl
44	84.5	4.8	700	1	US-08-726-525-7	Sequence 7, Appli
45	84.5	4.8	700	2	US-08-487-942-7	Sequence 7, Appli

ALIGNMENTS

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RESULT 1
US-08-241-465B-20
; Sequence 20, Application US/08241465B
; Patent No. 5719125
;  GENERAL INFORMATION:
;    APPLICANT:  Fujio SUZUKI
;    APPLICANT:  Yuji HIRAKI
;    APPLICANT:  Kazuhiro TAKAHASHI
;    APPLICANT:  Junko SUZUKI
;    APPLICANT:  Jun KONDO
;    APPLICANT:  Atsuko KOHARA
;    APPLICANT:  Akiko MORI
;    APPLICANT:  Ei YAMADA
;    TITLE OF INVENTION:  HUMAN CHONDROMODULIN-I PROTEIN
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      COUNTRY:  D.C.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/241,465B
;      FILING DATE:  May 11, 1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek, Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-8850
;      TELEFAX:
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  334 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-241-465B-20

  Query Match           29.9%;  Score 521;  DB 1;  Length 334;
  Best Local Similarity  35.5%;  Pred. No. 2.9e-42;
  Matches 119;  Conservative  62;  Mismatches 116;  Indels  38;  Gaps  12;
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Qy          6 PENCEDCHILNAEAF-----KSKKICKSLKICGLVFGILALTLIVLFW--GSKHFWPEVP 58
              |:: | |    :  |:      |     : ||:  :|  :::  :::||   |: :||
Db         15 PDDVEFC---SPPAYATLTVKPSSPARLLKVGAVV--LISGAVLLLFGAIGAFYFWKGSD 69

Qy         59 KKAYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQ 118
               |:: :|   ||: :   ||||     | |: |:| :| : |:||:|| ||| | | :
Db         70 SHIYNVHYTMSINGKLQDGSMEIDAGNNLETFKMGSGAEEAIAVNDFQNGITGIRFAGGE 129

Qy        119 KCFIKTQIKV-IPEF-SEPEEEID---ENEEITTTFFEQSVIWVPAEKPIENRDFLKNSK 173
              ||:|| |:|  |||  :  :: |    | : :   : | |:|||  ::|:::  || |||
Db        130 KCYIKAQVKARIPEVGAVTKQSISSKLEGKIMPVKYEENSLIWVAVDQPVKDNSFL-NSK 188

Qy        174 ILEICDNVTMYWINPTLISVSELQDFEEEGEDLHFPANEKK-----------GIEQNEQW 222
              :||:| :: ::|: ||      |:|     |       |    |:            |   ||
Db        189 VLELCGDLPIFWLKPTY--PKEIQRERREVVRKIVPTTTKRPHSGPRSNPGAGRLNNE-- 244

Qy        223 VVPQVKVEKTRHARQASEEELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEP 282
              | |: :      ||   : | :     : ||| ||  | ||| |||   :|:::|||
Db        245 TRPSVQEDS-----QAFNPDNPYHQQEGESMTFDPRLDHEGICCIECRRSYTHCQKICEP 299

Qy        283 LLGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV 317
              | ||||:|| ||| |  |||||||:|||||:|| |
Db        300 LGGYYPWPYNYQGCRSACRVIMPCSWWVARILGMV 334
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RESULT 2
US-08-241-465B-19
; Sequence 19, Application US/08241465B
; Patent No. 5719125
; GENERAL INFORMATION:
; APPLICANT: Fujio SUZUKI
; APPLICANT: Yuji HIRAKI
; APPLICANT: Kazuhiro TAKAHASHI
; APPLICANT: Junko SUZUKI
; APPLICANT: Jun KONDO
; APPLICANT: Atsuko KOHARA
; APPLICANT: Akiko MORI
; APPLICANT: Ei YAMADA
; TITLE OF INVENTION: HUMAN CHONDROMODULIN-I PROTEIN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,465B
; FILING DATE: May 11, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-241-465B-19

Query Match 29.6%; Score 516; DB 1; Length 334;
Best Local Similarity 35.2%; Pred. No. 8.9e-42;

Matches 118; Conservative 63; Mismatches 116; Indels 38; Gaps 12;

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Qy          6 PENCEDCHILNAEAF-----KSKKICKSLKICGLVFGILALTLIVLFW--GSKHFWPEVP 58
              |:: | |    :  |:      |     : ||:  :|  :::  :::||   |: :||
Db         15 PDDVEFC---SPPAYATLTVKPSSPARLLKVGAVV--LISGAVLLLFGAIGAFYFWKGSD 69

Qy         59 KKAYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQ 118
               |:: :|   ||: :   ||||     | |: |:| :| : |:||:|| ||| | | :
Db         70 SHIYNVHYTMSINGKLQDGSMEIDAGNNLETFKMGSGAEEAIAVNDFQNGITGIRFAGGE 129

Qy        119 KCFIKTQIKV-IPEF-SEPEEEID---ENEEITTTFFEQSVIWVPAEKPIENRDFLKNSK 173
              ||:|| |:|  |||  :  :: |    | : :   : | |:|||  ::|:::  || :||
Db        130 KCYIKAQVKARIPEVGAVTKQSISSKLEGKIMPVKYEENSLIWVAVDQPVKDNSFL-SSK 188

Qy        174 ILEICDNVTMYWINPTLISVSELQDFEEEGEDLHFPANEKK-----------GIEQNEQW 222
              :||:| :: ::|: ||      |:|     |       |    |:            |   ||
Db        189 VLELCGDLPIFWLKPTY--PKEIQRERREVVRKIVPTTTKRPHSGPRSNPGAGRLNNE-- 244

Qy        223 VVPQVKVEKTRHARQASEEELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEP 282
              | |: :      ||   : | :     : ||| ||  | ||| |||   :|:::|||
Db        245 TRPSVQEDS-----QAFNPDNPYHQQEGESMTFDPRLDHEGICCIECRRSYTHCQKICEP 299

Qy        283 LLGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV 317
              | ||||:|| ||| |  |||||||:|||||:|| |
Db        300 LGGYYPWPYNYQGCRSACRVIMPCSWWVARILGMV 334
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RESULT 3
US-08-241-465B-21
; Sequence 21, Application US/08241465B
; Patent No. 5719125
; GENERAL INFORMATION:
; APPLICANT: Fujio SUZUKI
; APPLICANT: Yuji HIRAKI
; APPLICANT: Kazuhiro TAKAHASHI
; APPLICANT: Junko SUZUKI
; APPLICANT: Jun KONDO
; APPLICANT: Atsuko KOHARA
; APPLICANT: Akiko MORI
; APPLICANT: Ei YAMADA
; TITLE OF INVENTION: HUMAN CHONDROMODULIN-I PROTEIN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,465B
; FILING DATE: May 11, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 296 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-241-465B-21

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  Query Match             24.7%;  Score 431;  DB 1;  Length 296;
  Best Local Similarity   31.2%;  Pred. No. 1.3e-33;
  Matches  103;  Conservative   57;  Mismatches  104;  Indels   66;  Gaps   11;

Qy          6 PENCEDCHILNAEAP-----KSKKICKSLKICGLVFGILALTLIVLFW--GSKHFWPEVP 58
              |:: | |   :  |:     |     : ||:  :|  :::  :::||   |: :||
Db         15 PDDVEFC---SPPAYATLTVKPSSPARLLKVGAVV--LISGAVLLLFGAIGAFYFWKGSD 69

Qy         59 KKAYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQ 118
                |:: :|   ||: :   ||||     | |: |:| :| : |:||:|
Db         70 SHIYNVHYTMSINGKLQDGSMEIDAGNNLETFKMGSGAEEAIAVNDFQN---------- 118

Qy        119 KCFIKTQIKVIPEFSEPEEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEIC 178
                    : |::|                  : | |:|||  ::|:::  || :||:||:|
Db        119 ------EGKIMP---------------VKYEENSLIWVAVDQPVKDNSFL-SSKVLELC 155

Qy        179 DNVTMYWINPTLISVSELQDFEEEGEDLHFPANEKK----------GIEQNEQWVVPQV 227
               :: : |: ||     |:|     |     |   |:           |   ||    | |
Db        156 GDLPISWLKPTY--PKEIQRERREVVRKIVPTTTKRPHNGPRSNPGAGRLNNE--TRPSV 211

Qy        228 KVEKTRHARQASEEELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYY 287
               : :      ||   : | :     : ||| ||  | ||| |||   :|:::|||| |||
Db        212 QEDS-----QAFNPDNPYHQQEGESMTFDPRLDHEGICCIECRRSYTHCQKICEPLGGYY 266

Qy        288 PYPYCYQGGRVICRVIMPCNWWVARMLGRV 317
              |:|| ||| |  |||||||:|||||:|| |
Db        267 PWPYNYQGCRSACRVIMPCSWWVARILGMV 296


RESULT 4
US-08-047-033-2
; Sequence 2, Application US/08047033
; Patent No. 5444157
;  GENERAL INFORMATION:
;    APPLICANT:  Fujio SUZUKI et al.
;    TITLE OF INVENTION:  CHONDROMODULIN-I PROTEIN
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 500 Kb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  DisplayWrite
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/047,033
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/821,859
;      FILING DATE:
;      APPLICATION NUMBER:  US/07/745,497
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-8850
;      TELEFAX:  202-371-8856
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:
;    ANTI-SENSE:
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;      ORGANISM:  bovine
;      STRAIN:
;      INDIVIDUAL ISOLATE:
;      DEVELOPMENTAL STAGE:
;      HAPLOTYPE:
;      TISSUE TYPE:  fetal cartilage
;      CELL TYPE:
;      CELL LINE:
;      ORGANELLE:
;    IMMEDIATE SOURCE:
;      LIBRARY:
;      CLONE:
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:
;      MAP POSITION:
;      UNITS:
;    FEATURE:
;      NAME/KEY:  modified site
;      LOCATION:  7
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:  /note= "Xaa is Met or Val"
;    FEATURE:
;      NAME/KEY:  modified site
;      LOCATION:  10
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:  /note= "Xaa is Glu or Thr"
;    FEATURE:
;      NAME/KEY:  modified site
;      LOCATION:  83
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:  /note= "Xaa is Cys or Val"
;    PUBLICATION INFORMATION:
;      AUTHORS:
;      TITLE:
;      JOURNAL:
;      VOLUME:
;      ISSUE:
;      PAGES:
;      DATE:
;      DOCUMENT NUMBER:
;      FILING DATE:
;      PUBLICATION DATE:
;      RELEVANT RESIDUES IN SEQ ID NO:
US-08-047-033-2

  Query Match             14.6%;  Score 254.5;  DB 1;  Length 120;
  Best Local Similarity   53.9%;  Pred. No. 4.3e-17;
  Matches   48;  Conservative   11;  Mismatches   27;  Indels    3;  Gaps    2;

Qy        232 TRHARQASEEEL-PINDYTENG--IEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP 288
              || : |    |   | | | : |  : ||| ||  | ||| |||   :|::: ||| ||:|
Db         32 TRPSVQEDAEPFNPDNPYHQEGESMTFDPRLDHEGICCIECRRSYTHCQKIXEPLGGYHP 91

Qy        289 YPYCYQGGRVICRVIMPCNWWVARMLGRV 317
              :|| ||| |  |||||||:|||||:|| |
Db         92 WPYNYQGCRSACRVIMPCSWWVARILGMV 120


RESULT 5
US-08-047-033-1
; Sequence 1, Application US/08047033
; Patent No. 5444157
;  GENERAL INFORMATION:
;    APPLICANT:  Fujio SUZUKI et al.
;    TITLE OF INVENTION:  CHONDROMODULIN-I PROTEIN
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack
;      STREET:  805 Fifteenth Street, N.W., #700
```

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;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  U.S.A.
;       ZIP:  20005
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 5.25 inch, 500 Kb
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  MS-DOS
;       SOFTWARE:  DisplayWrite
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/047,033
;       FILING DATE:
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/821,859
;       FILING DATE:
;       APPLICATION NUMBER:  US/07/745,497
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Warren M. Cheek Jr.
;       REGISTRATION NUMBER:  33,367
;       REFERENCE/DOCKET NUMBER:
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-8850
;       TELEFAX:  202-371-8856
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  121 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     HYPOTHETICAL:
;     ANTI-SENSE:
;     FRAGMENT TYPE:
;     ORIGINAL SOURCE:
;       ORGANISM:  bovine
;       STRAIN:
;       INDIVIDUAL ISOLATE:
;       DEVELOPMENTAL STAGE:
;       HAPLOTYPE:
;       TISSUE TYPE:  fetal cartilage
;       CELL TYPE:
;       CELL LINE:
;       ORGANELLE:
;     IMMEDIATE SOURCE:
;       LIBRARY:
;       CLONE:
;     POSITION IN GENOME:
;       CHROMOSOME/SEGMENT:
;       MAP POSITION:
;       UNITS:
;     FEATURE:
;       NAME/KEY:  modified site
;       LOCATION:  7
;       IDENTIFICATION METHOD:
;       OTHER INFORMATION:  /note= "Xaa is Met or Val"
;     FEATURE:
;       NAME/KEY:  modified site
;       LOCATION:  10
;       IDENTIFICATION METHOD:
;       OTHER INFORMATION:  /note= "Xaa is Glu or Thr"
;     FEATURE:
;       NAME/KEY:  modified site
;       LOCATION:  84
;       IDENTIFICATION METHOD:
;       OTHER INFORMATION:  /note= "Xaa is Cys or Val"
;     PUBLICATION INFORMATION:
;       AUTHORS:
;       TITLE:
;       JOURNAL:
;       VOLUME:
;       ISSUE:
;       PAGES:
;       DATE:
;       DOCUMENT NUMBER:
;       FILING DATE:
;       PUBLICATION DATE:
;       RELEVANT RESIDUES IN SEQ ID NO:
US-08-047-033-1

  Query Match             14.2%;  Score 248;  DB 1;  Length 121;
  Best Local Similarity   52.2%;  Pred. No. 1.9e-16;
  Matches   47;  Conservative   11;  Mismatches   28;  Indels    4;  Gaps    2;

Qy        232 TRHARQASEEEL-PINDYTE---NGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYY 287
              || : |   |   | | | :     : ||| ||  | ||| |||   :|::: ||| ||:
Db         32 TRPSVQEDAEPFNPDNPYHQQEGESMTFDPRLDHEGICCIECRRSYTHCQKIXEPLGGYH 91

Qy        288 PYPYCYQGGRVICRVIMPCNWWVARMLGRV 317
              |:|| ||| |  |||||||:|||||:|| |
Db         92 PWPYNYQGCRSACRVIMPCSWWVARILGMV 121


RESULT 6
US-09-107-532A-7138
; Sequence 7138, Application US/09107532A
; Patent No. 6583275
;   GENERAL INFORMATION:
;       APPLICANT: Lynn A Doucette-Stamm  and David Bush
;       TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                           ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;       NUMBER OF SEQUENCES: 7310
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;            STREET: 100 Beaver Street
;            CITY: Waltham
;            STATE: Massachusetts
;            COUNTRY: USA
;            ZIP: 02354
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD/ROM ISO9660
;            COMPUTER: PC
;            OPERATING SYSTEM: <Unknown>
;            SOFTWARE: ASCII
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/107,532A
;            FILING DATE: 30-Jun-1998
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/085,598
;            FILING DATE: 14 May 1998
;            APPLICATION NUMBER: 60/051571
;            FILING DATE: July 2, 1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ariniello, Pamela Deneke
;            REGISTRATION NUMBER: 40,489
;            REFERENCE/DOCKET NUMBER: GTC-012
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (781)893-5007
;            TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 7138:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 304 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       HYPOTHETICAL: YES
;       ORIGINAL SOURCE:
;            ORGANISM: Enterococcus faecium
;       FEATURE:
;            NAME/KEY:  misc_feature
;            LOCATION: (B) LOCATION 1...304
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7138:
US-09-107-532A-7138
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  Query Match             6.0%;  Score 105.5;  DB 4;  Length 304;
  Best Local Similarity   19.5%;  Pred. No. 0.043;
  Matches   55;  Conservative   48;  Mismatches  104;  Indels   75;  Gaps    9;

Qy         17 AEAFKSKKICKSLKI-CGLVFGILALTLIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEK- 74
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Db         25 AQIDKVYKKTKGVKLYLGAILGFLAIGMIIV------FSPYVVMGKSYDFETVKMSSAQNV 78

Qy         75 -KKIYMEIDPVT-----------------------------RTEIFRSGNGTDETLEVH 103
                 : | :| :                            :   : |  |   :|
Db         79 TSSLNMYVDDMEINREAGLFKLVLRYQDDTGTKSLSNIKSDYKLNFITNKNNEDVKTKVV 138

Qy        104 DFKNGYTGIYFVGLQKCFIKTQIKVIPEF----SEPEEEIDENE---------------- 143
                 : || ||:  | | |    : | | :     ||  :: | |
Db        139 KLSDEYTVIYYQNLPKDFGVISVTVNPRYIYPELEPSNDLKEKEIKFYAVDKDIKSNAKL 198

Qy        144 EITTTFFEQSVIWVPAEKPIEN--RDFLKNSKILEICDNVTMYWINPTLISVSELQDFEE 201
              |: :|   |   :   | |||  :|  |: : : : |                :| ::
Db        199 EVESTSDLQKDNFKYQIKAIENSIKDEKKSIEKMNLANKVVQ-------------KDIDK 245

Qy        202 EGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEEL 243
                ::| |   :::   :||   : |  :|  : : : || ::
Db        246 ANQNLEFQTLDEQTDTKNEISSM-QTTIENNKSSIEESENKI 286


RESULT 7
US-08-464-148-2
; Sequence 2, Application US/08464148
; Patent No. 5710026
;  GENERAL INFORMATION:
;    APPLICANT:  Sprecher, Cindy A.
;    TITLE OF INVENTION:  CYTOPLASMIC ANTIPROTEINASE-2 AND
;    TITLE OF INVENTION:  CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  Steuart Street Tower, One Market Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105-1493
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/464,148
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/385,500
;      FILING DATE:  08-FEB-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Parmelee, Steven W.
;      REGISTRATION NUMBER:  31,990
;      REFERENCE/DOCKET NUMBER:  13952-21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 467-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  374 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-464-148-2

  Query Match             5.6%;  Score 97.5;  DB 1;  Length 374;
  Best Local Similarity   21.3%;  Pred. No. 0.35;
  Matches   63;  Conservative   42;  Mismatches  112;  Indels   79;  Gaps   14;

Qy          7 ENCEDC--HILNAEAFKSKKICKSLKICGLVFGILALTLI--VLFWGSKHFWPEVPKKAY 62
              |: |:|  || :  | |::     :   | |  :  | |:  : | |    | |   : |
Db        123 EDTEECRKHINDWVAEKTEGKISEVLDAGTVDPLTKLVLVNAIYFKGK---WNEQFDRKY 179

Qy         63 DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFI 122
                 | :| ||| : |          :|:             || ||           :
Db        180 TRGMLFKTNEEKKTVQM---------MFKEAK----------FKMGYAD---------EV 211

Qy        123 KTQIKVIPEFSEPEEEI-------DENEEITTT----FFEQSVIWVPAEKPIENR--DFL 169
              ||:  :|     |||:        |:|  ::        :|:   |  :||  :::   ||
Db        212 HTQVLELPYV---EEELSMVILLPDDNTDLAVVEKALTYEKFKAWTNSEKLTKSKVQVFL 268

Qy        170 KNSKILEICDNVTMYWINPTLISVSELQDFEEEGEDLHFPANEKK----------GIEQN 219
                |: |        | : | |  :  :  |:|   |     : ||            :| |
Db        269 PRLKLEE------SYDLEPPFLRRLGMIDAFDEAKADFSGMSTEKNVPLSKVAHKCFVEVN 322

Qy        220 EQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPML----DERGYCCIYCRR 271
              |:          |::| :  |    |:        | |      :  | ::| |
Db        323 EEGTEAAAATAVVRNSRCSRMEPRFCADH--------PFLFFIRRHKTNCILFCGR 370


RESULT 8
US-08-385-500-2
; Sequence 2, Application US/08385500
; Patent No. 5712117
;  GENERAL INFORMATION:
;    APPLICANT:  Sprecher, Cindy A.
;    TITLE OF INVENTION:  CYTOPLASMIC ANTIPROTEINASE-2 AND
;    TITLE OF INVENTION:  CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  Steuart Street Tower, One Market Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105-1493
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/385,500
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Parmelee, Steven W.
;      REGISTRATION NUMBER:  31,990
;      REFERENCE/DOCKET NUMBER:  13952-21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 467-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  374 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-385-500-2

  Query Match             5.6%;  Score 97.5;  DB 1;  Length 374;
  Best Local Similarity   21.3%;  Pred. No. 0.35;
  Matches   63;  Conservative   42;  Mismatches  112;  Indels   79;  Gaps   14;

Qy          7 ENCEDC--HILNAEAFKSKKICKSLKICGLVFGILALTLI--VLFWGSKHFWPEVPKKAY 62
              |: |:|  || :  | |::     :   | |  :  | |:  : | |    | |   : |
Db        123 EDTEECRKHINDWVAEKTEGKISEVLDAGTVDPLTKLVLVNAIYFKGK---WNEQFDRKY 179

Qy         63 DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFI 122
                 | :| ||| : |          :|:             || ||           :
Db        180 TRGMLFKTNEEKKTVQM---------MFKEAK----------FKMGYAD---------EV 211

Qy        123 KTQIKVIPEFSEPEEEI-------DENEEITTT----FFEQSVIWVPAEKPIENR--DFL 169
```

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Db        212 HTQVLELPYV---EEELSMVILLPDDNTDLAVVEKALTYEKFKAWTNSEKLTKSKVQVFL 268

Qy        170 KNSKILEICDNVTMYWINPTLISVSELQDFEEEGEDLHFPANEKK----------GIEQN 219

Db        269 PRLKLEE------SYDLEPFLRRLGMIDAFDEAKADFSGMSTEKNVPLSKVAHKCFVEVN 322

Qy        220 EQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPML----DERGYCCIYCRR 271

Db        323 EEGTEAAAATAVVRNSRCSRMEPRFCADH--------PFLFFIRRHKTNCILFCGR 370
```

RESULT 9
US-08-846-784-2
; Sequence 2, Application US/08846784
; Patent No. 5747645
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,784
; FILING DATE: 30-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/385,500
; FILING DATE: 08-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-846-784-2

Query Match 5.6%; Score 97.5; DB 1; Length 374;
Best Local Similarity 21.3%; Pred. No. 0.35;
Matches 63; Conservative 42; Mismatches 112; Indels 79; Gaps 14;

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Qy          7 ENCEDC--HILNAEAFKSKKICKSLKICGLVFGILALTLI--VLFWGSKHFWPEVPKKAY 62

Db        123 EDTEECRKHINDWVAEKTEGKISEVLDAGTVDPLTKLVLVNAIYFKGK---WNEQFDRKY 179

Qy         63 DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFI 122

Db        180 TRGMLFKTNEEKKTVQM---------MFKEAK----------FKMGYAD---------EV 211

Qy        123 KTQIKVIPEFSEPEEEI-------DENEEITTT----FFEQSVIWVPAEKPIENR--DFL 169

Db        212 HTQVLELPYV---EEELSMVILLPDDNTDLAVVEKALTYEKFKAWTNSEKLTKSKVQVFL 268

Qy        170 KNSKILEICDNVTMYWINPTLISVSELQDFEEEGEDLHFPANEKK----------GIEQN 219

Db        269 PRLKLEE------SYDLEPFLRRLGMIDAFDEAKADFSGMSTEKNVPLSKVAHKCFVEVN 322

Qy        220 EQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPML----DERGYCCIYCRR 271

Db        323 EEGTEAAAATAVVRNSRCSRMEPRFCADH--------PFLFFIRRHKTNCILFCGR 370
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RESULT 10
US-09-134-001C-5242
; Sequence 5242, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5242
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5242

Query Match 5.3%; Score 92; DB 4; Length 384;
Best Local Similarity 26.4%; Pred. No. 1.2;
Matches 56; Conservative 36; Mismatches 62; Indels 58; Gaps 13;

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Qy         88 EIFRSGNGTDETLEVHDFKNG---YTGIYFVGLQKCFIKTQIKVIPEFSEPEEEIDENEE 144

Db        145 EIHRDGN-----IYTQNFKNGGIPATGLVKTGKTK---KTGTKVT---FKPDSEIFKS-- 191

Qy        145 ITTTF-FEQSVIWVPAEKPIENRDFLKNSKILEICDNVTMYWINPTLISVSELQDFEEEG 203

Db        192 -TTTFNFD-----ILSERLQESAFLLKDLK----------ITLTDLRSGKERE 228

Qy        204 EDLHFPANEKKGIEQNEQWV--VPQVKVEKTRHARQASEEELPI----ND-YTENGIEF- 255

Db        229 EIYHY----EEGIKEFVSYVNEGKEVLHDVTTFAGHSNGIEVDVAFQYNDQYSESILSFV 284

Qy        256 ------DPMLDERGYCCIYCRRGNRYCRRVCE 281

Db        285 NNVRTKDGGTHEVGFKTAMTRVFNEYARRINE 316
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RESULT 11
US-09-134-000C-4697
; Sequence 4697, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4697
; LENGTH: 899
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4697

Query Match 5.3%; Score 92; DB 4; Length 899;
Best Local Similarity 19.2%; Pred. No. 4.1;

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  Matches   53;  Conservative   40;  Mismatches   99;  Indels   84;  Gaps   12;

Qy         68 FYSNGEKKKI----YMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIK 123
              | :| :| ::    |   ||  :  : :   ||   :|| |      :||: :   | ::
Db        461 FTTNPKKVRLKSDDYFYADPEFKQRLSKVSKGT--IVEVEDLAYTQSGIFRLKTAKGYLT 518

Qy        124 TQIKVIPEF---------SEPEEEIDENEE--------------------ITTTFFEQSV 154
                 :: ::         | | : |  ||:                     :  |   |::
Db        519 ANKNIVEQYKGLEDTYYTSNPGQVITRNEDTYYKDVEFKTKANKVSAGSVLKVTAIEKTK 578

Qy        155 IWVPAEKPIENRDFLKNSKILEICDNVTMYWI------NPTLISVSELQDFEEEGEDLHF 208
               :|  |       |  |   :      |  ||       ||  | :    :|  : : |:
Db        579 SGIPRLKMANGYYFTANKNYVV----ATGSWIANYHTVNPGQIIMKNSDNFYGDSDFLY- 633

Qy        209 PANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPMLDERGYCCIY 268
                 ||   ::  :|| | :|                 | ||  :   :: : |    |
Db        634 -----KGAAVSKGSLVPVVGIE----------------YREN--QVPRLITQNG----Y 665

Qy        269 CRRGNRYCRRVCEPLLGY-YPYP---------YCYQ 294
                | ::|   :  | | ||        | ||
Db        666 LTANKSYAQKVVPNIKDYLYDYPEYVVMKTNDYYYQ 701


RESULT 12
US-09-068-569-2
; Sequence 2, Application US/09068569
; Patent No. 6238859
; GENERAL INFORMATION:
;  APPLICANT: Lke, Wolfgang
;  APPLICANT: Hunsmann, Gerhard
;  APPLICANT: Weber, Thomas
;  TITLE OF INVENTION: Virus Protein Antigens of the JC Virus
;  FILE REFERENCE: Luke et al
;  CURRENT APPLICATION NUMBER: US/09/068,569
;  CURRENT FILING DATE: 1998-07-17
;  EARLIER APPLICATION NUMBER: PCT/EP96/05177
;  EARLIER FILING DATE: 1996-11-22
;  EARLIER APPLICATION NUMBER: DE 195 43 553.2
;  EARLIER FILING DATE: 1995-11-22
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 354
;   TYPE: PRT
;   ORGANISM: JC virus
US-09-068-569-2

  Query Match             5.2%;  Score 91;  DB 3;  Length 354;
  Best Local Similarity   21.5%;  Pred. No. 1.4;
  Matches   61;  Conservative   27;  Mismatches   86;  Indels  110;  Gaps   15;

Qy         72 GEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIPE 131
              ||:|      |||   ::   |      :|| : | |   |  |   :||:      ||
Db          8 GERK------DPVQVPKLLIRGG-----VEVLEVKTGVDSITEV---ECFL------TPE 47

Qy        132 FSEPEEEI---DENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEI----------C 178
               :|:| :    ::  |: ||          |    ||| |    : |             |
Db         48 MGDPDEHLRGFSKSISISDTF----------ESDSPNRDMLPCYSVARIPLPNLNEDLTC 97

Qy        179 DNVTMYWINPTL----ISVSELQDFEEEGEDLH-------------------------- 207
               |: | |   ||    | |: | :    |:  |
Db         98 GNILM-WEAVTLKTEVIGVTSLMNVHSNGQATHDNGAGKPVQGTSFHFFSVGGEALELQG 156

Qy        208 --------------FPAN-----------EKKGIEQN-----EQWVVPQVKVEKTRH--A 235
                           || |           |  :::|     | ||    : | ||:
Db        157 VLFNYRTKYPDGTIFPKNATVQSQVMNTEHKAYLDKNKAYPVECWVPDPTRNENTRYFGT 216

Qy        236 RQASEEELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRV 279
                 |   |:    |        :||'| |    : |:  | |  |
Db        217 LTGGENVPPVLHITNTATTV--LLDEFGVGPL-CKGDNLYLSAV 257


RESULT 13
US-09-134-000C-5764
; Sequence 5764, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;  TITLE OF INVENTION:  ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 032796-032
;  CURRENT APPLICATION NUMBER: US/09/134,000C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/055,778
;  PRIOR FILING DATE: 1997-08-15
;  NUMBER OF SEQ ID NOS: 6812
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5764
;   LENGTH: 1096
;   TYPE: PRT
;   ORGANISM: Enterococcus faecalis
US-09-134-000C-5764

  Query Match             5.2%;  Score 90.5;  DB 4;  Length 1096;
  Best Local Similarity   19.3%;  Pred. No. 7.7;
  Matches   53;  Conservative   41;  Mismatches   86;  Indels   95;  Gaps   12;

Qy         50 SKHFWPEV-PKKAYDMEHTFY-------SNGEKKKIYMEIDPVTRTEIFRSG-------- 93
              :::|| |    : | :: | |         | ||  :    |   : :: | |
Db        577 NEYFWQETKAPEGYTLDETKYPVSIKKVDNNEKNAVITR-DVTAKEQVIRFGFDFFKFAG 635

Qy         94 --------------------NGTDETLEVHD-----------------FKNGYTGIYFV- 115
                                  ||:|    |                   |:|   | | :
Db        636 SADGTAETGFNDLSFKVSPLEGTNEITGAEDKATTACNEQLGFDGYGKFENLPYGDYLLE 695

Qy        116 ------GLQKCFIKTQIKVIPEFSEPEEEIDENEEITTTFFEQ-----SVIWVPAEKPIE 164
                   | ||    | :::   | | :::  ::| : |   |        :: || ||
Db        696 EIEAPEGFQKI---TPLEIRSTFKENKDDYAKSEYVFTITEEGQKQPIKMVTVPYEK--- 749

Qy        165 NRDFLKNSKILEICDNVTMYWINPTLISVSELQ------------DFEEEGEDLHFPANE 212
                 | |::     : : :| :     |:: |              || |  : | :  :|
Db        750 ----LTNNEFSVSLNRLMLYDLPEKEDSLTSLATWKDGNKKLNTLDFTELVDKLRYNLHE 805

Qy        213 KKGIEQNEQW--VVPQVKVEKTRHARQASEEELPI 245
                |     | |  |   : || |: |::  |:  |:
Db        806 IK-----EDWYVVAQAIDVEATKAAQEKDEKAKPV 835


RESULT 14
US-09-071-035-396
; Sequence 396, Application US/09071035
; Patent No. 6448043
;  GENERAL INFORMATION:
;    APPLICANT:  Gil H. Choi
;    TITLE OF INVENTION:  Enterococcus faecalis Polynucleotides and Polypeptides
;    NUMBER OF SEQUENCES:  496
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,035
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
```

```
;       NAME:  A. Anders Brookes
;       REGISTRATION NUMBER:  36,373
;       REFERENCE/DOCKET NUMBER:  PB369P2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (301) 309-8504
;       TELEFAX:  (301) 309-8512
;   INFORMATION FOR SEQ ID NO:  396:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  500 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-071-035-396

  Query Match             5.1%;  Score 88.5;  DB 4;  Length 500;
  Best Local Similarity   19.3%;  Pred. No. 3.9;
  Matches   53;  Conservative   40;  Mismatches   87;  Indels   95;  Gaps   12;

Qy         50 SKHFWPEV-PKKAYDMEHTFY-------SNGEKKKIYMEIDPVTRTEIFRSG-------- 93
              :::|| |    : | :: | |         | ||  :    |   : :: | |
Db         15 NEYFWQETKAPEGYTLDETKYPVSIKKVDNNEKNAVITR-DVTAKEQVIRFGFDFFKFAG 73

Qy         94 --------------------NGTDETLEVHD-----------------FKNGYTGIYFV- 115
                                  || |     |                 |:|   | | :
Db         74 SADGTAETGFNDLSFKVSPLEGTXEITGAEDKATTACNEQLGFDGYGKFENLPYGDYLLE 133

Qy        116 ------GLQKCFIKTQIKVIPEFSEPEEEIDENEEITTTFFEQ-----SVIWVPAEKPIE 164
                   | ||    | :::   | | :::  ::| : |   |        :: || ||
Db        134 EIEAPEGFQKI---TPLEIRSTFKENKDDYAKSEYVFTITEEGQKQPIKMVTVPYEK--- 187

Qy        165 NRDFLKNSKILEICDNVTMYWINPTLISVSELQ------------DFEEEGEDLHFPANE 212
                 | |::     : : :| :     |:: |              || |  : | :  :|
Db        188 ----LTNNEFSVSLNRLMLYDLPEKEDSLTSLATWKDGNKKLNTLDFTELVDKLRYNLHE 243

Qy        213 KKGIEQNEQW--VVPQVKVEKTRHARQASEEELPI 245
               |     | |  |   : || |: |::  |:  |:
Db        244 IK-----EDWYVVAQAIDVEATKAAQEKDEKAKPV 273


RESULT 15
US-09-071-035-358
; Sequence 358, Application US/09071035
; Patent No. 6448043
;  GENERAL INFORMATION:
;    APPLICANT:  Gil H. Choi
;    TITLE OF INVENTION:  Enterococcus faecalis Polynucleotides and Polypeptides
;    NUMBER OF SEQUENCES:  496
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,035
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  A. Anders Brookes
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PB369P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  358:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1074 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-071-035-358

  Query Match             5.1%;  Score 88.5;  DB 4;  Length 1074;
  Best Local Similarity   19.3%;  Pred. No. 12;
  Matches   53;  Conservative   40;  Mismatches   87;  Indels   95;  Gaps   12;

Qy         50 SKHFWPEV-PKKAYDMEHTFY-------SNGEKKKIYMEIDPVTRTEIFRSG-------- 93
              :::|| |    : | :: | |         | ||  :    |   : :: | |
Db        555 NEYFWQETKAPEGYTLDETKYPVSIKKVDNNEKNAVITR-DVTAKEQVIRFGFDFFKFAG 613

Qy         94 --------------------NGTDETLEVHD-----------------FKNGYTGIYFV- 115
                                  || |     |                 |:|   | | :
Db        614 SADGTAETGFNDLSFKVSPLEGTXEITGAEDKATTACNEQLGFDGYGKFENLPYGDYLLE 673

Qy        116 ------GLQKCFIKTQIKVIPEFSEPEEEIDENEEITTTFFEQ-----SVIWVPAEKPIE 164
                   | ||    | :::   | | :::  ::| : |   |        :: || ||
Db        674 EIEAPEGFQKI---TPLEIRSTFKENKDDYAKSEYVFTITEEGQKQPIKMVTVPYEK--- 727

Qy        165 NRDFLKNSKILEICDNVTMYWINPTLISVSELQ------------DFEEEGEDLHFPANE 212
                 | |::     : : :| :     |:: |              || |  : | :  :|
Db        728 ----LTNNEFSVSLNRLMLYDLPEKEDSLTSLATWKDGNKKLNTLDFTELVDKLRYNLHE 783

Qy        213 KKGIEQNEQW--VVPQVKVEKTRHARQASEEELPI 245
               |     | |  |   : || |: |::  |:  |:
Db        784 IK-----EDWYVVAQAIDVEATKAAQEKDEKAKPV 813


Search completed: March 30, 2004, 14:33:05
Job time : 23 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2004, 14:29:47 ; Search time 20 Seconds
(without alignments)
1524.636 Million cell updates/sec

Title: US-10-089-600-2
Perfect score: 1745
Sequence: 1 MAKNPPENCEDCHILNAEAF.....VICRVIMPCNWWVARMLGRV 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1745	100.0	317	2	JC7597	chondromodulin-I l
2	1694	97.1	317	2	JC7603	tenomodulin - mous
3	514.5	29.5	335	2	JT0569	chondromodulin-I p
4	492.5	28.2	333	2	JE0287	chondromodulin-I p
5	112.5	6.4	499	2	E96969	histidine kinase (
6	100.5	5.8	350	2	T34002	hypothetical prote
7	100	5.7	827	2	A90544	hypothetical prote
8	100	5.7	844	2	F86231	hypothetical prote
9	97.5	5.6	374	2	A59273	proteinase inhibit
10	97.5	5.6	799	2	C82929	ATP synthase alpha
11	97	5.6	655	2	A57681	hypothetical prote
12	96.5	5.5	732	2	S73089	glycosyltransferas
13	96	5.5	2109	1	A46309	genome polyprotein
14	95.5	5.5	622	2	A64494	hypothetical prote
15	95.5	5.5	752	2	H86770	hypothetical prote
16	95.5	5.5	837	2	JN0292	antigen 332 - mala
17	95.5	5.5	1090	2	H86806	hypothetical prote
18	95	5.4	1045	1	SYEXI	isoleucine-tRNA li
19	94.5	5.4	658	2	A64584	hypothetical prote
20	93.5	5.4	313	2	T19503	hypothetical prote
21	93	5.3	325	2	T18283	hypothetical prote
22	93	5.3	1429	2	T19422	hypothetical prote
23	92.5	5.3	198	2	A70013	sulfite oxidase ho
24	92	5.3	608	2	D72306	hypothetical prote
25	92	5.3	891	2	B84614	hypothetical prote
26	92	5.3	916	2	F71962	hypothetical prote
27	91.5	5.2	869	2	S76720	hypothetical prote
28	91.5	5.2	1056	1	GNLJG3	HIV-1 retropepsin
29	91	5.2	351	2	T43791	cystathionine beta
30	91	5.2	354	1	VVVP1J	coat protein VP1 -
31	90.5	5.2	985	2	T41135	hypothetical prote
32	90	5.2	452	2	D64583	hypothetical prote
33	90	5.2	505	2	B64560	poly E-rich protei
34	90	5.2	595	2	E69470	amino-acid ABC tra
35	90	5.2	692	1	P3XRPC	inner layer protei
36	90	5.2	920	2	T08853	protein phosphatas
37	90	5.2	1471	2	T19506	hypothetical prote
38	89.5	5.1	1054	1	GNLJG5	HIV-1 retropepsin
39	89.5	5.1	1233	2	S56271	hypothetical prote
40	89.5	5.1	1537	2	JC4172	DNA (cytosine-5-)-
41	89.5	5.1	1965	2	T33216	hypothetical prote
42	89	5.1	431	2	I51189	IFAPa-400 - chicke
43	89	5.1	1606	2	T34073	paranemin - chicke
44	89	5.1	1840	2	T29091	transitin - chicke
45	88.5	5.1	440	2	E71625	variant-specific s

ALIGNMENTS

RESULT 1
JC7597
chondromodulin-I like protein, ChM1L - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C;Accession: JC7597
R;Yamana, K.; Wada, H.; Takahashi, Y.; Sato, H.; Kasahara, Y.; Kiyoki, M.
Biochem. Biophys. Res. Commun. 280, 1101-1106, 2001
A;Title: Molecular cloning and characterization of ChM1L, a novel member molecule simil
A;Reference number: JC7597; MUID:21092728; PMID:11162640
A;Accession: JC7597
A;Molecule type: mRNA
A;Residues: 1-317 <YAM>
C;Comment: This protein is a novel type II transmembrane protein which is similar to ch
C;Genetics:
A;Gene: chm1l
A;Map position: Xq22
C;Keywords: transmembrane protein
F;31-50/Domain: transmembrane #status predicted <TMM>
F;265-317/Region: highly conserved

Query Match 100.0%; Score 1745; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 1.8e-126;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317
```

RESULT 2
JC7603

```
tenomodulin - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C;Accession: JC7603
R;Shukunami, C.; Oshima, Y.; Hiraki, Y.
Biochem. Biophys. Res. Commun. 280, 1323-1327, 2001
A;Title: Molecular cloning of tenomodulin, a novel chondromodulin-I related gene.
A;Reference number: JC7603; MUID:21092761; PMID:11162673
A;Contents: Embryo, 17-days
A;Accession: JC7603
A;Molecule type: mRNA
A;Residues: 1-317 <SHU>
A;Cross-references: GB:AF219993
C;Comment: Tenomodulin is a type II transmembrane protein on cell surface with an antian
C;Genetics:
A;Gene: TeM
C;Keywords: transmembrane protein
F;31-50/Domain: transmembrane #status predicted <TMM>
F;255-317/Region: conserved carboxyl-terminus, homologous to chondromodulin-I #status pr
F;265-306/Domain: antiangiogenic #status predicted <ANT>

  Query Match            97.1%;  Score 1694;  DB 2;  Length 317;
  Best Local Similarity  96.2%;  Pred. No. 1.5e-122;
  Matches  305;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              ||||||||||.||||||||.||||||||||||||||||||||||||||||||||||||||| ||
Db          1 MAKNPPENCEGCHILNAEALKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVSKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              |||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db         61 TYDMEHTFYSNGEKKKIYMEIDPITRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||:|||||||||:|||||||:|||||:|||||||||||||||||||:|||||
Db        181 VTMYWINPTLIAVSELQDFEEDGEDLHFPTSEKKGIDQNEQWVVPQVKVEKTRHTRQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EDLPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317


RESULT 3
JT0569
chondromodulin-I precursor - bovine
N;Alternate names: 18K glycoprotein, cartilage; SCGP; small cartilage-derived glycoprote
C;Species: Bos primigenius taurus (cattle)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 05-Nov-1999
C;Accession: JT0569; A33138; A36431
R;Hiraki, Y.; Tanaka, H.; Inoue, H.; Kondo, J.; Kamizono, A.; Suzuki, F.
Biochem. Biophys. Res. Commun. 175, 971-977, 1991
A;Title: Molecular cloning of a new class of cartilage-specific matrix, chondromodulin-I
A;Reference number: JT0569; MUID:91222210; PMID:1709014
A;Accession: JT0569
A;Molecule type: mRNA
A;Residues: 1-335 <HIR>
A;Cross-references: GB:M65081; NID:g162840; PIDN:AAA30445.1; PID:g162841
A;Note: part of this sequence, including the amino end of the mature protein, was determ
R;Neame, P.J.; Treep, J.T.; Young, C.N.
submitted to the Protein Sequence Database, October 1990
A;Reference number: A33138
A;Accession: A33138
A;Molecule type: protein
A;Residues: 215-220,'M',222,'NE',225-335 <NEA>
A;Note: 221-Val was also found
R;Neame, P.J.; Treep, J.T.; Young, C.N.
J. Biol. Chem. 265, 9628-9633, 1990
A;Title: An 18-kDa glycoprotein from bovine nasal cartilage. Isolation and primary stru
A;Reference number: A36431; MUID:90277643; PMID:2351661
A;Accession: A36431
A;Molecule type: protein
A;Residues: 215-220,'MNE',224-225,227-256,'D',257-335 <NE2>
A;Note: 221-Val was also found
A;Note: this sequence has been revised in reference A36535
R;Neame, P.J.; Treep, J.T.; Young, C.N.
J. Biol. Chem. 265, 22056, 1990
A;Reference number: A36535
A;Contents: annotation; sequence revision
C;Comment: This protein stimulates DNA synthesis of cultured growth-plate chondrocytes
C;Keywords: extracellular matrix; glycoprotein; transmembrane protein
F;43-59/Domain: transmembrane #status predicted <TMM>
F;215-335/Product: chondromodulin-I #status experimental <MAT>
F;223,236/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;244/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;283-287,284-324/Disulfide bonds: (or 283-324, 284-287) #status experimental
F;294-318,298-314/Disulfide bonds: #status experimental

  Query Match            29.5%;  Score 514.5;  DB 2;  Length 335;
  Best Local Similarity  33.0%;  Pred. No. 5e-32;
  Matches  115;  Conservative   60;  Mismatches  109;  Indels   65;  Gaps    8;

Qy          6 PENCEDCH--ILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKKAYD 63
              |:: | |      |  |     : ||: :|    |: |::    |: :||       |:
Db         15 PDDVEFCSPPAYAAVTVKPSSPARLLKVGAVVLISGAVLLLLGAIGAFYFWKGSDNHIYN 74

Qy         64 MEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIK 123
              : :|   ||: :   ||||     | |: |:| :| :||:||:|| ||| | | :||:||
Db         75 VHYTMSINGKLQDGSMEIDAGNNLETFKMGSGAEEAVEVNDFQNGITGIRFAGGEKCYIK 134

Qy        124 TQIKV-IPEF---------SEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSK 173
               |:|  |||          || | :|     :   : | |:|||  ::|::: || :||
Db        135 AQVKARIPEVGTMTKQSISSELEGKI-----MPVKYEENSLIWVAGDQPVKDNSFL-SSK 188

Qy        174 ILEICDNVTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTR 233
              :||:| :: ::|: ||                  :|    | |::  : :| ::    |
Db        189 VLELCGDLPIFWLKPT-----------------YP----KEIQRERRELVRKIVTTTTT 226

Qy        234 HARQASEEELPINDYTENG------------------------IEFDPMLDERGYCCIY 268
              ::  :  |      ||                        : ||| ||  | |||
Db        227 RRLRSGPQGTPAPGRPNNGTRPSVQEDAEPFNPDNPYHQQEGESMTFDPRLDHEGICCIE 286

Qy        269 CRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV 317
              |||  :|:::|||| ||:|:|| ||| |  |||||||:|||||:|| |
Db        287 CRRSYTHCQKICEPLGGYHPWPYNYQGCRSACRVIMPCSWWVARILGMV 335


RESULT 4
JE0287
chondromodulin-I precursor [similarity] - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: JE0287
R;Shukunami, C.; Hiraki, Y.
Biochem. Biophys. Res. Commun. 249, 885-890, 1998
A;Title: Expression of cartilage-specific functional matrix chondromodulin-I mRNA in ra
A;Reference number: JE0287; MUID:98401184; PMID:9731231
A;Accession: JE0287
A;Molecule type: mRNA
A;Residues: 1-333 <SHU>
A;Cross-references: DDBJ:AF072129; NID:g3641531; PIDN:AAC36470.1; PID:g3641532
C;Keywords: extracellular matrix; glycoprotein; transmembrane protein
F;43-59/Domain: transmembrane #status predicted <TMM>
F;215-333/Product: chondromodulin-I #status predicted <MAT>
F;223/Binding site: carbohydrate (Thr) (covalent) #status predicted
F;243/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;281-285,282-322,292-316,296-312/Disulfide bonds: #status predicted

  Query Match            28.2%;  Score 492.5;  DB 2;  Length 333;
```

```
  Best Local Similarity   33.4%;  Pred. No. 2.4e-30;
  Matches  110;  Conservative   72;  Mismatches  120;  Indels   27;  Gaps   12;

Qy          6 PENCEDCHILNAEAFKSKKI-----CKSLKICGLVFGILALTLIVLFW--GSKHFWPEVP 58
              |:: | |       |: :  :      : ||:  :|  :::  :::||   |: : |
Db         15 PDDVEFC---GPPAYATVTVKPSGPARLLKVGAVV--LISGAVLLLFGAIGAFYLWKGSD 69

Qy         59 KKAYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQ 118
                |:: :|   ||: :   ||||      | |: |:| :| :||:||:|| ||| | | :
Db         70 NHIYNVHYTMSINGKLQDGSMEIDARNNLETFKMGSGAEEAIEVNDFQNGITGIRFAGGE 129

Qy        119 KCFIKTQIKV-IPEF-SEPEEEID---ENEEITTTFFEQSVIWVPAEKPIENRDFLKNSK 173
              ||:|| |:|  :||  :  :: |    | : :      |::::||   :|:::  || :::
Db        130 KCYIKAQVKARVPEVGTVTQQSISSELEGKIMPVKHEEEALVWVAVGQPVQDNSFL-SAR 188

Qy        174 ILEICDNVTMYWINPTLISVSELQDFEEEGEDLHFPANEKK---GIEQNEQWVVPQVKVE 230
              :||:| :: ::|: ||     |:|     |       |    |:    |    |      ::: :
Db        189 VLELCGDLPIFWLKPTY--PKEIQRERREVVRKTVPTTTKRPHSGPRGNPG--PARMRND 244

Qy        231 KTRHARQASEEELPINDYTENG--IEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP 288
                  ::  ||    | | | : |  : ||| ||  | ||| |||   :|:::|||| || |
Db        245 SRPSVQEDSEPFNPDNPYHQEGESMTFDPRLDHEGICCIECRRSYTHCQKICEPLGGYNP 304

Qy        289 YPYCYQGGRVICRVIMPCNWWVARMLGRV 317
              :|| ||| |  |||:|||:|||||:|| |
Db        305 WPYNYQGCRSACRVVMPCSWWVARILGMV 333


RESULT 5
E96969
histidine kinase (HAMP, HisKA and HATPase domains) [imported] - Clostridium acetobutylic
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: E96969
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: E96969
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-499 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK78544.1; PID:g15023432; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0565

  Query Match             6.4%;  Score 112.5;  DB 2;  Length 499;
  Best Local Similarity   22.3%;  Pred. No. 0.59;
  Matches   71;  Conservative   49;  Mismatches  103;  Indels   95;  Gaps   21;

Qy         15 LNAEAFKSKKICKSLKI-CGLVFGILALTLIVL------FWGSKHFWPEVP--------- 58
              |   :|  ||: ||:::   : |||  |   :|      ::  ||   ||
Db          9 LKLYSFSKKKVVKSIRLELVVTFGICLLAAFILGSWYTGYYNDKHMMAEVDYSSGIQRIS 68

Qy         59 ------------KKAYDMEHTFYSNGEKK--KIYMEIDPVTRTE---IFRSGNGTDETLE 101
                         | : |  :   :| |   |:|:     | ||   :|:| |  :: ::
Db         69 SDMEDLKGMLDGKNSSDEINKMIDSGAKDDIKVYL-----TDTEGKVLFKSSNAKEKKID 123

Qy        102 VHD-------FKNGYTGIYFVGLQKCFIKTQIKVIPEFSEPEEEID----ENEE---ITT 147
              :||       ||  |      :      ||  | :  |  |   |||    :|:       | :
Db        124 IHDLIVKSEKFKREYDKATVINTVNGIIKKTISL--ESVEQYNEIDGIKIDNKNAYIIVS 181

Qy        148 TFFEQSVIWV-PAEKPIENRDFLKNSKILEICDNVTMYW------------INPTLISVS 194
                :| : :: |   |      ||  | |: :   | :::            ::  |: :|
Db        182 GIPKQKITYIRPGYSP-----FL--SGIIAVITFVFIFYFLTNRKMEYIESVSNGLVEIS 234

Qy        195 ELQ-DFE--EEGEDLHFPANEKKGIEQNEQWVVP--QVKVEKTRHARQASEEELPINDYT 249
              :  |:     |||       | | :   |    : ::|| | | :         ||
Db        235 KGNLDYRIMLMGED------ELKNLADNINSMASELQKRIEKEREAEKTK------NDLI 282

Qy        250 ENGIEFD---PMLDERGY 264
                | :  |   |:   :||
Db        283 TN-VSHDLRTPLTSVKGY 299


RESULT 6
T34002
hypothetical protein W03G1.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34002
R;Pauley, A.; Scheet, P.; Harper, M.
submitted to the EMBL Data Library, February 1999
A;Description: The sequence of C. elegans cosmid W03G1.
A;Reference number: Z21454
A;Accession: T34002
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-350 <PAU>
A;Cross-references: EMBL:AF125964; PIDN:AAD14750.1; GSPDB:GN00022; CESP:W03G1.2
A;Experimental source: strain Bristol N2; clone W03G1
C;Genetics:
A;Gene: CESP:W03G1.2
A;Map position: 4
A;Introns: 19/3; 97/1; 233/3; 335/3

  Query Match             5.8%;  Score 100.5;  DB 2;  Length 350;
  Best Local Similarity   20.9%;  Pred. No. 3.1;
  Matches   52;  Conservative   40;  Mismatches   72;  Indels   85;  Gaps   13;

Qy         50 SKHFWPEVPKKAY-----------DMEHTFY-SNGEKKKIYMEIDPVTRTEIFRSGNGT 96
              ||      |||| |           |   ||| :|  |||:   : ||         :
Db        145 SKLLMDRVPKKPYRLKNKPDGMMLCDEPSTFYRTNTSKKKLKTSLLPVE--------DSY 196

Qy         97 DETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIW 156
              |   :: | |                                 |||::: : ::: |       |
Db        197 DHVRKLEDIK-------------------------KEPEQDVYKGQDVPT--------W 222

Qy        157 VPAEKPIENRDFLKNSKILEI-CDNVTMY--------WINPTLISVSELQDFEE--EGED 205
                  :| :: |  :  : : :  |:: ||         | || : ::|||   |  : ::
Db        223 AVKIEPTDD-DMKETDEAITVSTDHLEMYRNKKLSLKSIPPTKLVLNELQPLVELKKRDE 281

Qy        206 LHFPANEKKGIEQNEQWVVPQVKVEKT----RHARQASEEELPINDYTENGIEFDPMLDE 261
              :||              |  :|    :          ||  |: ::  ::|::  ::||    |
Db        282 VHF-----------ETGLVFSNTIRSLLLVHESARALSDGKVD-DEYSDKKVQFDTQEPE 329

Qy        262 RGYCCIYCR 270
                |  || |
Db        330 ATY--IYSR 336


RESULT 7
A90544
hypothetical protein MYPU_2570 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: A90544
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: A90544
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-827 <KUR>
A;Cross-references: GB:AL445566; PID:g14089670; PIDN:CAC13430.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPU_2570
A;Genetic code: SGC3
C;Superfamily: valine-tRNA ligase

  Query Match             5.7%;  Score 100;  DB 2;  Length 827;
  Best Local Similarity   21.8%;  Pred. No. 10;
```

```
  Matches   57;  Conservative   45;  Mismatches   67;  Indels   92;  Gaps   14;

Qy          24 KICKSLKICGLVFGILALTLIVLFWGSKHFWPEVP-------KKAYD---MEHTFYSNGE 73
               ||  |::    ::|  | | |           | :|        |  ||    :||||    |
Db         634 KITKNIDFQKVIFKRLLLLL----------HPFIPFLTDHLFKIIYDQELLEHTF----E 679

Qy          74 KKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIPEFS 133
                ||:        :|:     |  |: : |                        |: | ||
Db         680 NKKL--------KTQ----KNNVDQLILV----------------------IRAIREFR 704

Qy         134 EPEEEIDENEEITTTFFEQSVIWVP----AEKPIENRDFL------KNSKILEICDNVTM 183
               | : :| : |:|          |:      :: |:  :||      :||: : | :|: :
Db         705 E-KYQISKKEKIK--------YWIQDCQFLQEDIDAINFLTFSELSQNSENMTIVENIKI 755

Qy         184 YWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWV--VPQVKVEKTRHARQASEE 241
               : | |  |  :  ::  :: | | |     : :  ||:::   | :|||          ||
Db         756 FMILPKNIEENLSKEKAQKIEFLKFEIKRAQSLLLNEKFISKAPTLKVE---------EE 806

Qy         242 ELPINDYTENGIEFDPMLDER 262
               :  :  |    ::   :|||:
Db         807 KAKLEKYQ---LQLKELLDEK 824


RESULT 8
F86231
hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: F86231
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: F86231
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-844 <STO>
A;Cross-references: GB:AE005172; NID:g2160167; PIDN:AAB60730.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
C;Superfamily: myb-related protein cdc5; myb DNA-binding repeat homology

  Query Match             5.7%;  Score 100;  DB 2;  Length 844;
  Best Local Similarity   22.7%;  Pred. No. 10;
  Matches   58;  Conservative   36;  Mismatches   88;  Indels   74;  Gaps   12;

Qy          90 FRSGNGTDETLEVHD---------------FKNGYTGIYFVGLQKCFIKTQIKVIP---E 131
               ||      :| :::|:                ::| |      || :   : ||   |   |
Db         447 FRDELHINEDMDMHESAKLERQRREEARRSLRSGLT-----GLPQPKNEYQIVAQPPPEE 501

Qy         132 FSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFL-KNSKILE-------------- 176
               ||||:|:|:           :    ||:     :  | | ||:|:
Db         502 SEEPEEKIEED-------MSDRIARERAEEEARQQALLKKRSKVLQRDLPRPPAASLAVI 554

Qy         177 -----ICDNVTMYWINPTLISVSELQDFEE-----EGEDLHFPANEKKGIEQNEQWVVPQ 226
                    |       : || | |::    ||      | ::  :| ::|           :
Db         555 RNSLLSADGDKSSVVPPTPIEVADKMVREELLQLLEHDNAKYPLDDK----------AEK 604

Qy         227 VKVEKTRHARQASEEELPINDYTENGI-EFDPMLDERG-YCCIYCRRGNR------YCRR 278
               |  | |  | || : | |:|: || : | | |: | | : |:     |:
Db         605 KKGAKNRTNRSAS-QVLAIDDFDENELQEADKMIKEEGKFLCVSMGHENKTLDDFVEAHN 663

Qy         279 VCEPLLGYYPYPYCYQ 294
               |   | |:|    |:
Db         664 TCVNDLMYFPTRSAYE 679


RESULT 9
A59273
proteinase inhibitor 8 - human
N;Alternate names: cytoplasmic antiproteinase 2 (CAP-2)
C;Species: Homo sapiens (man)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 15-Sep-2003
C;Accession: A59273
R;Sprecher, C.A.; Morgenstern, K.A.; Mathewes, S.; Dahlen, J.R.; Schrader, S.K.; Foster
J. Biol. Chem. 270, 29854-29861, 1995
A;Title: Molecular cloning, expression, and partial characterization of two novel membe
A;Reference number: A59273; MUID:96102039; PMID:8530382
A;Accession: A59273
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-374 <SPR>
A;Cross-references: GB:L40377; NID:g1160926; PIDN:AAC41939.1; PID:g1160927
A;Experimental source: tissue type placenta; note (vector lambda gt11); gene CAP2
C;Genetics:
A;Gene: GDB:PI8; CAP2
A;Cross-references: GDB:599392; OMIM:601697
A;Map position: 18q21.3-18q21.3
C;Superfamily: Serpin
C;Keywords: proteinase inhibitor
F;339/Inhibitory site: Arg (unidentified proteinase) #status predicted

  Query Match             5.6%;  Score 97.5;  DB 2;  Length 374;
  Best Local Similarity   21.3%;  Pred. No. 5.8;
  Matches   63;  Conservative   42;  Mismatches  112;  Indels   79;  Gaps   14;

Qy           7 ENCEDC--HILNAEAFKSKKICKSLKICGLVFGILALTLI--VLFWGSKHFWPEVPKKAY 62
               |: |:|  || :  | |::     :   | |  :  | |:  : | |    | |   : |
Db         123 EDTEECRKHINDWVAEKTEGKISEVLDAGTVDPLTKLVLVNAIYFKGK---WNEQFDRKY 179

Qy          63 DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFI 122
                    | :| ||| : |       :|:          || ||           :
Db         180 TRGMLFKTNEEKKTVQM---------MFKEAK----------FKMGYAD---------EV 211

Qy         123 KTQIKVIPEFSEPEEEI-------DENEEITTT----FFEQSVIWVPAEKPIENR--DFL 169
                 ||: .:|     |||:       |:| ::       :|:   |  :|| :::   ||
Db         212 HTQVLELPYV---EEELSMVILLPDDNTDLAVVEKALTYEKFKAWTNSEKLTKSKVQVFL 268

Qy         170 KNSKILEICDNVTMYWINPTLISVSELQDFEEEGEDLHFPANEKK----------GIEQN 219
                  |: |       | : | |  :  :  |:|   |    : ||           :| |
Db         269 PRLKLEE------SYDLEPFLRRLGMIDAFDEAKADFSGMSTEKNVPLSKVAHKCFVEVN 322

Qy         220 EQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPML----DERGYCCIYCRR 271
               |:          |:| :  |     |:        | |       :  | ::| |
Db         323 EEGTEAAAATAVVRNSRCSRMEPRFCADH--------PFLFFIRRHKTNCILFCGR 370


RESULT 10
C82929
ATP synthase alpha chain UU132 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: C82929
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mi
A;Reference number: A82870
A;Accession: C82929
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-799 <GLA>
A;Cross-references: GB:AE002114; GB:AF222894; NID:g6899086; PIDN:AAF30538.1; GSPDB:GN00
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: atpA-2; UU132
A;Genetic code: SGC3

  Query Match             5.6%;  Score 97.5;  DB 2;  Length 799;
  Best Local Similarity   20.7%;  Pred. No. 15;
```

```
  Matches   57;  Conservative   42;  Mismatches   79;  Indels   97;  Gaps   12;

Qy          44 IVLFWGSKHFWPEVP-------------------------KKAYDMEHT---------- 67
               |:||    :    |:||                        |||:| |:|
Db         436 IILFTVKEKLIPQVPVERIQDFKEYLLNYFKGTKLRADLEDKKAFDKENTPAFRCAIQKA 495

Qy          68 ---FYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKT 124
                 | :| :  |   | :     : |      :|:: | | :| :           ||
Db         496 INSFLNNSQDFKPCEEAEQTAFDKFFNE----NESIVV-DGENDFN----------FINE 540

Qy         125 QIKVIP--------------EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPI------ 163
               :: : |              :| ||:| :: |:      ||:    |  || |
Db         541 EVSLKPTTETSEAVQIEEKVQDFVEPQEILETNKMEENHIFEE----VEPEKIICEHHEF 596

Qy         164 ---ENRDFLKNSKILEICDNVTMYWINPTLISVSELQDFEEEGEDLH--FPANEKKGIE- 217
                  ||:: ::  ::||  |    | |  |:    |: : | : :||    |  | :  |
Db         597 EIAENQEKIEGQQVLE--DTNHEYSIYETVEQSGEVDNDESKDDDLEVLVPVAEIEHDEA 654

Qy         218 -----QNEQWV-----VPQVKVEKTRHARQASEEE 242
                    :|  ||     | :|: :   :  ::| |
Db         655 ILDERENRNWVFSDSAVSEVEKQTIMISISSNEAE 689


RESULT 11
A57681
hypothetical protein - Mycoplasma capricolum
C;Species: Mycoplasma capricolum
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 07-Dec-1999
C;Accession: A57681
R;Zhu, P.P.; Reizer, J.; Peterkofsky, A.
Protein Sci. 3, 2115-2128, 1994
A;Title: Unique dicistronic operon (ptsI-crr) in Mycoplasma capricolum encoding enzyme I
ncing, promoter analysis, and protein characterization.
A;Reference number: A57681; MUID:95218642; PMID:7703858
A;Accession: A57681
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-655 <RES>
A;Cross-references: EMBL:U15110; NID:g602679; PIDN:AAA70404.1; PID:g602684
C;Genetics:
A;Genetic code: SGC3

  Query Match             5.6%;  Score 97;  DB 2;  Length 655;
  Best Local Similarity   21.3%;  Pred. No. 13;
  Matches   57;  Conservative   44;  Mismatches   99;  Indels   68;  Gaps   12;

Qy           7 ENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKKAYDMEH 66
               :| ||       |  :|| |                          :|  :|:  |
Db         155 DNIEDIDDSKLEILESKYI----------------------PNQHNYPDYVKN------ 185

Qy          67 TFYSNGEKKKIYMEIDPVTRT----------EIFRSGNGTDETLEVHDFKNGYTGIYFVG 116
                 :      ::|| |:    | :           :  :| ||   |: | : |  | |
Db         186 --FKTVSAEEIYKELYDRTFSIKFLVKLKDGGLLSNGTGTGWLLDYHKYSN--TNKY--- 238

Qy         117 LQKCFIKTQIKVIPEFSEPEEEIDENEEITTTFFEQS---VIWVPAEKPIENRDFLKNSK 173
                 | || | : |: :||    : ::|:|   ::: |   || :   |       || : :
Db         239 --KMPIATNLHVLADFSNSLTD-EQNKEF--NYYDPSGNKVIGLGLGKADNVTDFSRKNN 293

Qy         174 ILEICDNVTMYWINPTLISVSELQDFEEEGEDLHFPANE-KKGIEQNEQWVVPQVKVEKT 232
                 :  :|:  |::|          ||||   ::  :  |:  ||| :  : |   |   |
Db         294 NSKSENNIANYYLNN--------QDFENYLKNDFWSVNKFSKGISE-PKIVFGAVDFMKD 344

Qy         233 R----HARQASEEELPINDYTENGIEFD 256
               |    |     :| :   :| :|  | :
Db         345 RAIKNHYEALQKEAINYYNYKKNNNEIN 372


RESULT 12
S73089
glycosyltransferase (EC 2.4.1.-) - Sulfolobus solfataricus
N;Alternate names: protein c0622
C;Species: Sulfolobus solfataricus
C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 17-Mar-1999
C;Accession: S73089
R;Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S.
Mol. Microbiol. 22, 175-191, 1996
A;Title: Organizational characteristics and information content of an archaeal genome: 1
A;Reference number: S73076; MUID:97055432; PMID:8899719
A;Accession: S73089
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-732 <SEN>
A;Cross-references: EMBL:Y08256; NID:g1707679; PID:e284015; PID:g1707701
A;Experimental source: strain P2
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996
C;Keywords: glycosyltransferase; hexosyltransferase

  Query Match             5.5%;  Score 96.5;  DB 2;  Length 732;
  Best Local Similarity   20.4%;  Pred. No. 16;
  Matches   64;  Conservative   51;  Mismatches  114;  Indels   85;  Gaps   15;

Qy          37 GILALTLIVLFWGSKHFWPEVPKKAYDMEHTFYSN---------GEKKKIYMEIDPVTRT 87
               ||:  |          : :  | :  |  |:     |  |           : ::  : ||
Db         393 GIMRL---------QQYMPAIFAKGYEDTTLFIYNRLISLNEVGSDLRRFSLSIDDFHNF 443

Qy          88 EIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIPEFSEPEEE--------- 138
                    |    :  ||  || |                  :: :| |: |  :  ||
Db         444 NQSRVNTISMNTLSTHDTKFSED----------VRARISVLSEIPKEWEERVIYWHDLL 492

Qy         139 ---IDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICD-NVTMYWINPTLISVS 194
                  ||:|:|     | |::  | : :  :|:: :||  |  | :  |   | || :   :
Db         493 RPNIDKNDEYR---FYQTL--VGSYEGFDNKERIKNHMIKVIREAKVHTTWENPNIEYEN 547

Qy         195 ELQDFEEEG-EDLHFPANEKKGIEQNEQWV----------------VPQV--KVEKTRH 234
               :: || :|  |: :|  |: :  |:   :                  || :    | |
Db         548 KVLDFIDEAFENSNF-RNDFESFEKKIVYFGYMKSLVATTLKFLSPGVPDIYQGTEVWRF 606

Qy         235 ARQASEEELPI---------NDYTENGIEF-DPMLDERGYCCIYCRRGNRYCRRVCEPLL 284
                     :  :|:          |: ||  :|  || :       :| ::  :  |     |
Db         607 LLTDPDNRMPVDFKKLRELLNNLTEKNLELSDPRVK-----MLYVKKLLQLRREY--SLN 659

Qy         285 GYYPYPYCYQGGRV 298
                 | | |: :| |:|
Db         660 DYKPLPFGFQRGKV 673


RESULT 13
A46309
genome polyprotein - vesicular stomatitis New Jersey virus (strain Ogden)
N;Alternate names: RNA nucleotidyltransferase (RNA-directed); RNA replicase
N;Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C;Species: vesicular stomatitis New Jersey virus
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 11-Jun-1999
C;Accession: A46309
R;Barik, S.; Rud, E.W.; Luk, D.; Banerjee, A.K.; Kang, C.Y.
Virology 175, 332-337, 1990
A;Title: Nucleotide sequence analysis of the L gene of vesicular stomatitis virus (New J

A;Reference number: A46309; MUID:90177235; PMID:2155516
A;Accession: A46309
A;Molecule type: genomic RNA
A;Residues: 1-2109 <BAR>
A;Cross-references: GB:M29788; NID:g336029; PIDN:AAA48442.1; PID:g336030
C;Genetics:
A;Gene: L
C;Superfamily: rhabdovirus L protein
C;Keywords: nucleotidyltransferase; RNA binding; RNA biosynthesis; RNA replication
F;530-549/Region: RNA binding #status predicted

  Query Match             5.5%;  Score 96;  DB 1;  Length 2109;
  Best Local Similarity   22.1%;  Pred. No. 67;
  Matches   52;  Conservative   46;  Mismatches   91;  Indels   46;  Gaps   13;

Qy          55 PEVPKKAYDMEHTFYSNGEKKKIYMEIDPV-TRTEIFRSGNGTDETLEVH-DFKN-GYTG 111
               |::||  :  ||      |  :::    : :  |  ::  |     |  | |:  |:: |:
Db         306 PKIPKFPHFEEHV---KGSVQELTQRSNRIQTLYDLIMSMKDVDLVLVVYGSFRHWGHPF 362
```

```
Qy        112 I-YFVGLQKCFIKTQIKVIPEFSEPEEEIDEN--EEITTTF--------FEQSVIWV--- 157
              | || ||:|  : ||: :       |: ||:   ::: :          | :|  |
Db        363 IDYFQGLEK--LHTQVNM-------EKHIDKEYPQQLASDLARLVLNKQFSESKKWFVDP 413

Qy        158 -------PAEKPIENRDFLKNSKILEICDNVTMYWINPTLISVSELQDFEEEG---EDLH 207
                    |  : : |: :   :|| :  ||    |    ||   |: | :     |
Db        414 SKMSPKHPFYEHVINKTWPTAAKIQDFGDN----WHKLPLIQCFEIPDLIDPSVIYSDKS 469

Qy        208 FPANEKKGIE---QNEQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPML 259
                |:|: |:        :|  || :|    :|:  :  : |  |||:: | ::
Db        470 HSMNKKEVIQHVRSKPNIPIPSNKVLQTMLTNRATNWKAFLKDIDENGLDDDDLI 524


RESULT 14
A64494
hypothetical protein MJ1554 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: A64494
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: A64494
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-622 <BUL>
A;Cross-references: GB:U67596; GB:L77117; NID:g2826430; PIDN:AAB99574.1; PID:g1500447; T
C;Genetics:
A;Map position: FOR1529328-1531196
C;Superfamily: hypothetical protein MJ1554

  Query Match             5.5%;  Score 95.5;  DB 2;  Length 622;
  Best Local Similarity   22.0%;  Pred. No. 16;
  Matches   56;  Conservative   40;  Mismatches   79;  Indels   79;  Gaps   13;

Qy         21 KSKKICKSLKICGLVFGILALTLIVLFWGSKHFW----PEVPKKAYDMEHTFYSNGEKKK 76
              |  || |::  || :: :    ||||: |      :    ||:||  : |:     ||
Db        132 KYAKIIKNISECGYLY-LTNNTLIVISWNKITSYNVSNPEMPKIIWQMD----LNGS--- 183

Qy         77 IYMEIDPVTRTEIFRSGNGT----------DETLEVHDFKNGYTGIYF------------ 114
               |::          |  |||          |  :  :::| ||   |
Db        184 -YVD---------SRLYNGTLYLVVRKNSIDCPIVWNNYKIGYDKYYIPELPPIYSMDFD 233

Qy        115 -------VGLQKCFIKTQIKVIPEFSEP-----------EEEIDENEEITTTFFEQSVI 155
                    : ::   ::  | ::  :                 :|:| : :     | :
Db        234 TTYIISRINIKSGKVENSIAIVGNYKTTLYMSKNNLYFAYNLKINEKKLMLNFLNESADK 293

Qy        156 WVPAE------KPIENRDFLKNSKILEICDNVTMYWINPTLIS------VSELQ-DFEEE 202
              : | |      : ||| ||  |:| :|| : :  |    :| |      : :|| |||
Db        294 YFPTEVADKIKRVIENEDFGDNAKFVEITETIERYL--SSLPSEKRHNLMKKLQNDFENY 351

Qy        203 GEDLHFPANEKKGI 216
               |: |:   |  ||
Db        352 LEE-HWEEPEYTGI 364


RESULT 15
H86770
hypothetical protein yliB [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: H86770
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: H86770
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-752 <STO>
A;Cross-references: GB:AE005176; PID:g12724133; PIDN:AAK05266.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: yliB

  Query Match             5.5%;  Score 95.5;  DB 2;  Length 752;
  Best Local Similarity   21.7%;  Pred. No. 20;
  Matches   63;  Conservative   37;  Mismatches   95;  Indels   95;  Gaps   17;

Qy         16 NAEAFKSKKICKSLK-ICGLV----FGILALTLIVLFWGSKH-FWPEVPKK-AYDMEH-- 66
              | :   :  :||::| :|  |      |   :| |    |: | ||  :     || |
Db        174 NTQLIPTLTMCKAIKELCPSVKHIQLGGNFITRISSLIGNLHPFWNYIDSMLLYDGEENL 233

Qy         67 -TFYSNGEKKKIYMEID---------PVTRTEIFRSG--NGTDETLEVHDFKNGYTGIYF 114
               :|    | | | |           : | ||  |    |       :  ||  :|   :
Db        234 SSFLQQLENNKDYSNIPNLYYLDDHRNLKRNEIVESKTINSLPPDFDGFDFSKYFTDNLW 293

Qy        115 VGL---QKCFIKTQIKVIPEFS------EPEEEIDENEEITT--------TFFEQSVIWV 157
              : :   : |  |:    ||  |        | ::: || |:          :| ::: : |
Db        294 IPIYTSRACVNKSTFCTIPNASGGKFRHMPAKKVVENMEVVKEKYGISHFSFVDETFL-V 352

Qy        158 PAEKPI-------ENRD--------FLK------------------------NSKILEI 177
              | | |       | :|        | |                        | ::|::
Db        353 PKMKQIAKLLIDNEQKDISWYCETRFSKLLTADTTQILRKGGCSNIQFGLESYNQRVLDL 412

Qy        178 CD-NVTMYWINPTLISVSE-------------LQDFEEEGEDLHFPANE 212
              | |: : || | :|:  |               :  ||      || |||
Db        413 MDKNIDIAWIEPNIINCFEAGISVHLFFMTGFPTETLEEAKNTYHF-ANE 461


Search completed: March 30, 2004, 14:33:39
Job time : 22 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2004, 14:29:47 ; Search time 17 Seconds
(without alignments)
970.955 Million cell updates/sec

Title: US-10-089-600-2
Perfect score: 1745
Sequence: 1 MAKNPPENCEDCHILNAEAF.....VICRVIMPCNWWVARMLGRV 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1745	100.0	317	1	TNMD_HUMAN	Q9h2s6 homo sapien
2	1694	97.1	317	1	TNMD_MOUSE	Q9ep64 mus musculu
3	1657	95.0	317	1	TNMD_RAT	Q9esc2 rattus norv
4	553	31.7	347	1	CHM1_CHICK	Q9puu8 gallus gall
5	529	30.3	334	1	CHM1_RAT	O70367 rattus norv
6	518	29.7	334	1	CHM1_MOUSE	Q9z1f6 mus musculu
7	516	29.6	334	1	CHM1_HUMAN	O75829 homo sapien
8	514.5	29.5	335	1	CHM1_BOVIN	P17404 bos taurus
9	492.5	28.2	333	1	CHM1_RABIT	O77770 oryctolagus
10	403.5	23.1	286	1	CHM1_BRARE	P58239 brachydanio
11	97.5	5.6	374	1	SPB8_HUMAN	P50452 homo sapien
12	97	5.6	655	1	YKDA_MYCCA	P45615 mycoplasma
13	96	5.5	2109	1	RRPL_VSVJO	P16379 vesicular s
14	95.5	5.5	622	1	YF54_METJA	Q58949 methanococc
15	95	5.4	312	1	SPR2_CAEEL	Q18240 caenorhabdi
16	95	5.4	1044	1	SYI_METTM	P26499 methanobact
17	94.5	5.4	681	1	MP10_HUMAN	O00566 homo sapien
18	93	5.3	632	1	KU70_CHICK	O93257 gallus gall
19	93	5.3	682	1	TDR5_HUMAN	Q8nat2 homo sapien
20	92.5	5.3	684	1	HTPG_PORGI	Q9s3q2 porphyromon
21	92	5.3	664	1	PARE_STAEP	Q8csn9 staphylococ
22	91.5	5.2	1056	1	POL_SIVM1	P05896 simian immu
23	91	5.2	354	1	COA1_POVJC	P03089 polyomaviru
24	90	5.2	692	1	VP3_ROTPC	P26192 porcine rot
25	89.5	5.1	1054	1	POL_SIVMK	P05897 simian immu
26	89.5	5.1	1233	1	YFI6_YEAST	P43597 saccharomyc
27	89.5	5.1	1537	1	DNM1_CHICK	Q92072 gallus gall
28	89	5.1	864	1	41_HUMAN	P11171 homo sapien
29	89	5.1	1001	1	RPGR_MOUSE	Q9r0x5 mus musculu
30	88	5.0	351	1	FEN_SULTO	Q976h6 sulfolobus
31	87.5	5.0	149	1	RNP_MUSPA	Q9qyx3 mus pahari
32	87.5	5.0	634	1	YG74_METJA	Q59068 methanococc
33	87	5.0	1409	1	COPI_DROME	P04146 drosophila
34	87	5.0	2820	1	NF1_RAT	P97526 rattus norv
35	86.5	5.0	283	1	Y635_METJA	Q58052 methanococc
36	86.5	5.0	699	1	HS82_ARATH	P55737 arabidopsis
37	86.5	5.0	699	1	HS83_ARATH	P51818 arabidopsis
38	86	4.9	606	1	SPB4_YEAST	P25808 saccharomyc
39	86	4.9	700	1	HS9C_DICDI	P54651 dictyostel
40	85.5	4.9	493	1	ECX1_METMA	Q8ptt8 methanosarc
41	85.5	4.9	660	1	SYR_MOUSE	Q9d0i9 mus musculu
42	85.5	4.9	661	1	SYR_CRILO	P37880 cricetulus
43	85	4.9	350	1	IPYR_CAEEL	Q18680 caenorhabdi
44	85	4.9	414	1	Y288_MYCGE	P47530 mycoplasma
45	85	4.9	442	1	TIG_BUCAI	P57546 buchnera ap

ALIGNMENTS

RESULT 1
TNMD_HUMAN
ID TNMD_HUMAN STANDARD; PRT; 317 AA.
AC Q9H2S6; Q9HBX0; Q9UJG0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tenomodulin (TeM) (hTeM) (Chondromodulin-I like protein) (ChM1L)
DE (hChM1L) (Myodulin).
GN TNMD OR CHM1L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092728; PubMed=11162640;
RA Yamana K., Wada H., Takahashi Y., Sato H., Kasahara Y., Kiyoki M.;
RT "Molecular cloning and characterization of ChM1L, a novel membrane
RT molecule similar to chondromodulin-I.";
RL Biochem. Biophys. Res. Commun. 280:1101-1106(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092761; PubMed=11162673;
RA Shukunami C., Oshima Y., Hiraki Y.;
RT "Molecular cloning of tenomodulin, a novel chondromodulin-I related
RT gene.";
RL Biochem. Biophys. Res. Commun. 280:1323-1327(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Cros N., Tkatchenko A.V., Leclerc L., Leger J.J., Marini J.-F.,
RA Dechesne C.A.;
RT "Gene expression alterations revealed by suppression subtractive
RT hybridization in rat soleus muscle disuse atrophy.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE OF 61-307 FROM N.A.
RA Lawlor S.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: May be an angiogenesis inhibitor.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the chondromodulin-I family.
CC -!- SIMILARITY: Contains 1 BRICHOS domain.
CC --
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CC --
DR EMBL; AB055421; BAB21756.1; -.
DR EMBL; AF234259; AAG49144.1; -.
DR EMBL; AF191770; AAG28395.1; -.

```
DR   EMBL; AL035608; CAB55680.1; -.
DR   PIR; JC7597; JC7597.
DR   InterPro; IPR007084; BRICHOS.
DR   Pfam; PF04089; BRICHOS; 1.
DR   PROSITE; PS50869; BRICHOS; 1.
KW   Glycoprotein; Transmembrane; Signal-anchor.
FT   DOMAIN        1     30       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     31     50       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       51    317       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN       93    186       BRICHOS.
FT   CARBOHYD     94     94       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    180    180       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     40     40       A -> T (IN REF. 3).
FT   CONFLICT     71     71       N -> S (IN REF. 3).
FT   CONFLICT    192    192       S -> SGTFAKQLHHNFAFIIL (IN REF. 4).
SQ   SEQUENCE   317 AA;  37130 MW;  D17507D7E2EA0C68 CRC64;

  Query Match             100.0%;  Score 1745;  DB 1;  Length 317;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-124;
  Matches  317;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317


RESULT 2
TNMD_MOUSE
ID   TNMD_MOUSE     STANDARD;      PRT;   317 AA.
AC   Q9EP64;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Tenomodulin (TeM) (mTeM) (Chondromodulin-I like protein) (ChM1L)
DE   (mChM1L) (Myodulin).
GN   TNMD OR CHM1L.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21092728; PubMed=11162640;
RA   Yamana K., Wada H., Takahashi Y., Sato H., Kasahara Y., Kiyoki M.;
RT   "Molecular cloning and characterization of ChM1L, a novel membrane
RT   molecule similar to chondromodulin-I.";
RL   Biochem. Biophys. Res. Commun. 280:1101-1106(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21092761; PubMed=11162673;
RA   Shukunami C., Oshima Y., Hiraki Y.;
RT   "Molecular cloning of tenomodulin, a novel chondromodulin-I related
RT   gene.";
RL   Biochem. Biophys. Res. Commun. 280:1323-1327(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/10ScSn; TISSUE=Skeletal muscle;
RA   Cros N., Tkatchenko A.V., Leclerc L., Leger J.J., Marini J.-F.,
RA   Dechesne C.A.;
RT   "Gene expression alterations revealed by suppression subtractive
RT   hybridization in rat soleus muscle disuse atrophy.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: May be an angiogenesis inhibitor.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: Highly expressed in eye, skeletal muscle and
CC       rib.
CC   -!- DEVELOPMENTAL STAGE: Expression begins at day 11 and is maintained
CC       during the development of embryo.
CC   -!- SIMILARITY: Belongs to the chondromodulin-I family.
CC   -!- SIMILARITY: Contains 1 BRICHOS domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB055422; BAB21757.1; -.
DR   EMBL; AF219993; AAG48938.1; -.
DR   EMBL; AF191768; AAG28393.1; -.
DR   EMBL; BC006919; AAH06919.1; -.
DR   PIR; JC7603; JC7603.
DR   MGD; MGI:1929885; Tnmd.
DR   InterPro; IPR007084; BRICHOS.
DR   Pfam; PF04089; BRICHOS; 1.
DR   PROSITE; PS50869; BRICHOS; 1.
KW   Glycoprotein; Transmembrane; Signal-anchor.
FT   DOMAIN        1     30       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     31     50       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       51    317       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN       93    186       BRICHOS.
FT   CARBOHYD     94     94       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    180    180       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   317 AA;  37047 MW;  D7A00952F2E2ED9D CRC64;

  Query Match             97.1%;  Score 1694;  DB 1;  Length 317;
  Best Local Similarity   96.2%;  Pred. No. 1.5e-120;
  Matches  305;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;
```

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Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              |||||||||| |||||||| ||||||||||||||||||||||||||||||||||||||| ||
Db          1 MAKNPPENCEGCHILNAEALKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVSKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              |||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db         61 TYDMEHTFYSNGEKKKIYMEIDPITRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||:|||||||||:||||||| :|||||:|||||||||||||||| |||||
Db        181 VTMYWINPTLIAVSELQDFEEDGEDLHFPTSEKKGIDQNEQWVVPQVKVEKTRHTRQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EDLPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317
```

```
RESULT 3
TNMD_RAT
ID   TNMD_RAT       STANDARD;      PRT;   317 AA.
AC   Q9ESC2;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Tenomodulin (TeM) (rTeM) (Chondromodulin-I like protein) (ChM1L)
DE   (rChM1L) (Myodulin).
GN   TNMD OR CHM1L.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Skeletal muscle;
RX   MEDLINE=21092728; PubMed=11162640;
RA   Yamana K., Wada H., Takahashi Y., Sato H., Kasahara Y., Kiyoki M.;
RT   "Molecular cloning and characterization of ChM1L, a novel membrane
RT   molecule similar to chondromodulin-I.";
RL   Biochem. Biophys. Res. Commun. 280:1101-1106(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Cros N., Tkatchenko A.V., Leclerc L., Leger J.J., Marini J.-F.,
RA   Dechesne C.A.;
RT   "Gene expression alterations revealed by suppression subtractive
RT   hybridization in rat soleus muscle disuse atrophy.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: May be an angiogenesis inhibitor.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC   -!- SIMILARITY: Belongs to the chondromodulin-I family.
CC   -!- SIMILARITY: Contains 1 BRICHOS domain.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF191769; AAG28394.1; -.
DR   EMBL; AB055423; BAB21758.1; -.
DR   InterPro; IPR007084; BRICHOS.
DR   Pfam; PF04089; BRICHOS; 1.
DR   PROSITE; PS50869; BRICHOS; 1.
KW   Glycoprotein; Transmembrane; Signal-anchor.
FT   DOMAIN        1     30       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     31     50       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       51    317       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN       93    186       BRICHOS.
FT   CARBOHYD     94     94       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    180    180       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   317 AA;  36971 MW;  8C0328825F915D88 CRC64;

  Query Match             95.0%;  Score 1657;  DB 1;  Length 317;
  Best Local Similarity   94.6%;  Pred. No. 9.1e-118;
  Matches  300;  Conservative    7;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              |||||||||| |||||||| ||||| |||||||||||||||||||||||||||||||| ||
Db          1 MAKNPPENCEGCHILNAEALKSKKIRKSLKICGLVFGILALTLIVLFWGSKHFWPEVSKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              | |||||||||||||| |||||:|||||||||||||||||||||||||||||||||||||
Db         61 TYGMEHTFYSNGEKKKISMEIDPITRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||:|||||||||:||||||| :|||||:|||||||||||||||| |||||
Db        181 VTMYWINPTLIAVSELQDFEEDGEDLHFPTSEKKGIDQNEQWVVPQVKVEKTRRTRQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              |:||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EDLPVNDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317
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RESULT 4
CHM1_CHICK
ID   CHM1_CHICK     STANDARD;      PRT;   347 AA.
AC   Q9PUU8; Q9YI63;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Chondromodulin-I precursor (ChM-I) (Leukocyte cell-derived chemotaxin
DE   1) [Contains: Chondrosurfactant protein (CH-SP)].
GN   LECT1 OR CHM1.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20058447; PubMed=10590475;
RA   Dietz U.H., Ziegelmeier G., Bittner K., Bruckner P., Balling R.;
RT   "Spatio-temporal distribution of Chondromodulin-I mRNA in the chicken
RT   embryo: Expression during cartilage development and formation of the
RT   heart and eye.";
RL   Dev. Dyn. 216:233-243(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=White leghorn; TISSUE=Fetal sternum;
RX   MEDLINE=99379620; PubMed=10452551;
RA   Shukunami C., Yamamoto S., Tanabe T., Hiraki Y.;
RT   "Generation of multiple transcripts from the chicken chondromodulin-I
RT   gene and their expression during embryonic development.";
RL   FEBS Lett. 456:165-170(1999).
CC   -!- FUNCTION: Bifunctional growth regulator. May contribute to the
CC       rapid growth of cartilage and vascular invasion prior to the
CC       replacement of cartilage by bone during endochondral bone
CC       development (By similarity).
```

```
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and secreted. Accumulated in the
CC       inter-territorial matrix of cartilage (By similarity).
CC   -!- TISSUE SPECIFICITY: Expressed in the cartilage and in fetal
CC       precartilaginous tissues as well as in heart and eye.
CC   -!- DEVELOPMENTAL STAGE: Expression onset occurs between stage 10 and
CC       stage 13.
CC   -!- PTM: After cleavage, the post-translationally modified ChM-I is
CC       secreted as a glycoprotein (By similarity).
CC   -!- SIMILARITY: Belongs to the chondromodulin-I family.
CC   -!- SIMILARITY: Contains 1 BRICHOS domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF138280; AAD32212.1; -.
DR   EMBL; AF027380; AAD08642.1; -.
DR   InterPro; IPR007084; BRICHOS.
DR   Pfam; PF04089; BRICHOS; 1.
DR   PROSITE; PS50869; BRICHOS; 1.
KW   Glycoprotein; Transmembrane; Cleavage on pair of basic residues;
KW   Chondrogenesis.
FT   CHAIN         1    209       CHONDROSURFACTANT PROTEIN
FT                                (BY SIMILARITY).
FT   PROPEP      210    213       POTENTIAL.
FT   CHAIN       214    347       CHONDROMODULIN-I.
FT   TRANSMEM     45     65       POTENTIAL.
FT   DOMAIN      103    200       BRICHOS.
FT   DISULFID    295    299       BY SIMILARITY.
FT   DISULFID    296    336       BY SIMILARITY.
FT   CARBOHYD    256    256       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    250    250       D -> E (IN REF. 2).
SQ   SEQUENCE   347 AA;  38636 MW;  F3C5FF338E5D4B66 CRC64;

  Query Match           31.7%;  Score 553;  DB 1;  Length 347;
  Best Local Similarity   39.2%;  Pred. No. 1.5e-34;
  Matches  120;  Conservative   54;  Mismatches   96;  Indels   36;  Gaps    8;

Qy         40 ALTLIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDET 99
              || |:    |: :||   :: |:: :|   ||: :  ||||    | |::|:|::|
Db         50 ALLLLAGAIGAFYFWKATERQVYNVHYTMSINGKVQDGSMEIDAGNNLETFKTGSGSEEA 109

Qy        100 LEVHDFKNGYTGIYFVGLQKCFIKTQIKV-IPEF---------SEPEEEIDENEEITTTF 149
              :|||||: | ||| | | :||:|| | |  :||          |: |:||     :   |
Db        110 VEVHDFQIGITGIRFAGGEKCYIKAQPKARVPEVDAMTKASLSSDLEDEI-----MPVRF 164

Qy        150 FEQSVIWVPAEKPIENRDFLKNSKILEICDNVTMYWINPTLISVSELQDFE----EEGED 205
              | |:||| |::||::  || : ||||:| :: ::|: ||     : :  |    :   :
Db        165 DENSLIWVAADEPIKHNGFL-SPKILELCGDLPIFWLRPTYPKDKQRERREMKRNKRQSE 223

Qy        206 LHFPA----------NEKKGIEQNEQWVVPQVKVEKTRHARQASEEEL----PINDYTEN 251
               :| |          | :    | | : ||    :|| :| |::  |    | |
Db        224 SNFDAEHRAAAAEEVNTRSTPTQLTQDLGPQ--SNETRPMQQESDQTLNPDNPYNQLEGE 281

Qy        252 GIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWVA 311
              |: ||||||  | ||| |||    |:|:|||||||||:|| ||| |  ||:||||:||||
Db        282 GMAFDPMLDHLGVCCIECRRSYTQCQRICEPLLGYYPWPYNYQGCRTACRIIMPCSWWVA 341

Qy        312 RMLGRV 317
              |::| |
Db        342 RIMGVV 347


RESULT 5
CHM1_RAT
ID   CHM1_RAT       STANDARD;      PRT;   334 AA.
AC   O70367;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Chondromodulin-I precursor (ChM-I) (Leukocyte cell-derived chemotaxin
DE   1) [Contains: Chondrosurfactant protein (CH-SP)].
GN   LECT1 OR CHMI.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar Kyoto; TISSUE=Cartilage;
RX   MEDLINE=21226558; PubMed=11328727;
RA   Funaki H., Sawaguchi S., Yaoeda K., Koyama Y., Yaoita E., Funaki S.,
RA   Shirakashi M., Oshima Y., Shukunami C., Hiraki Y., Abe H.,
RA   Yamamoto T.;
RT   "Expression and localization of angiogenic inhibitory factor,
RT   chondromodulin-I, in adult rat eye.";
RL   Invest. Ophthalmol. Vis. Sci. 42:1193-1200(2001).
CC   -!- FUNCTION: Bifunctional growth regulator that stimulates the growth
CC       of cultured chondrocytes in the presence of basic fibroblast
CC       growth factor (FGF) but inhibits the growth of cultured vascular
CC       endothelial cells. May contribute to the rapid growth of cartilage
CC       and vascular invasion prior to the replacement of cartilage by
CC       bone during endochondral bone development (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and secreted. Accumulated in the
CC       inter-territorial matrix of cartilage (By similarity).
CC   -!- PTM: After cleavage, the post-translationally modified ChM-I is
CC       secreted as a glycoprotein (By similarity).
CC   -!- SIMILARITY: Belongs to the chondromodulin-I family.
CC   -!- SIMILARITY: Contains 1 BRICHOS domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF051425; AAC05574.1; -.
DR   InterPro; IPR007084; BRICHOS.
DR   Pfam; PF04089; BRICHOS; 1.
DR   PROSITE; PS50869; BRICHOS; 1.
KW   Glycoprotein; Transmembrane; Cleavage on pair of basic residues;
KW   Chondrogenesis.
FT   CHAIN         1    210       CHONDROSURFACTANT PROTEIN
FT                                (BY SIMILARITY).
FT   PROPEP      211    214       BY SIMILARITY.
FT   CHAIN       215    334       CHONDROMODULIN-I (BY SIMILARITY).
FT   TRANSMEM     46     66       POTENTIAL.
FT   DOMAIN      105    201       BRICHOS.
FT   DISULFID    282    286       BY SIMILARITY.
FT   DISULFID    283    323       BY SIMILARITY.
FT   CARBOHYD    243    243       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   334 AA;  37386 MW;  DB865E515952A4CD CRC64;

  Query Match           30.3%;  Score 529;  DB 1;  Length 334;
  Best Local Similarity   36.6%;  Pred. No. 9.5e-33;
  Matches  120;  Conservative   62;  Mismatches  122;  Indels   24;  Gaps   11;

Qy          6 PENCEDCHILNAEAFKSKKICKS------LKICGLVFGILALTLIVLFW--GSKHFWPEV 57
              ||: | |   :  |: :  :  |       ||:  :|  :::  :::||    |: :||
Db         15 PEDVEFC---SPPAYATVTVKPSGSPTRLLKVGAVV--LISGAVLLLFGAIGAFYFWKGN 69

Qy         58 PKKAYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGL 117
                 |:: :|   ||  :   ||||      | |: |:| :| :||:||:|| ||| | |
Db         70 DNHIYNVHYTMSINGRLQDASMEIDAANNLETFKMGSGAEEAIEVNDFQNGITGIRFAGG 129

Qy        118 QKCFIKTQIKV-IPEFSE-PEEEIDENEE--ITTTFFEQSVIWVPAEKPIENRDFLKNSK 173
              :||:|| |:|  ||| |   :: | | |   :   : | |:|||  ::|:::  || :||
Db        130 EKCYIKAQVKARIPEVSTGTKQSISELEGKIMPVKYEENSLIWVAVDQPVKDNSFL-SSK 188

Qy        174 ILEICDNVTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTR 233
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Db        189 ILEFCGDLPIFWLKP--MYPKEIPRERREVVRSSAPSTTRRPHSEPRGNAGPGRLSNRTR 246

Qy        234 HARQASEEEL-PINDYTE---NGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPY 289

Db        247 PSVQDDEEPFNPDNPYHQQEGESMTFDPRLDHEGICCIECRRSYTHCQKICEPLGGYYPW 306

Qy        290 PYCYQGGRVICRVIMPCNWWVARMLGRV 317

Db        307 PYNYQGCRSACRVVMPCSWWVARILGMV 334


RESULT 6
CHM1_MOUSE
ID   CHM1_MOUSE     STANDARD;      PRT;   334 AA.
AC   Q9Z1F6; Q9CXU5;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Chondromodulin-I precursor (ChM-I) (Leukocyte cell-derived chemotaxin
DE   1) [Contains: Chondrosurfactant protein (CH-SP)].
GN   LECT1 OR CHMI.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hiraki Y., Shukunami C., Inoue H., Suzuki F.;
RL   Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryonic head;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- FUNCTION: Bifunctional growth regulator that stimulates the growth
CC       of cultured chondrocytes in the presence of basic fibroblast
CC       growth factor (FGF) but inhibits the growth of cultured vascular
CC       endothelial cells. May contribute to the rapid growth of cartilage
CC       and vascular invasion prior to the replacement of cartilage by
CC       bone during endochondral bone development (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and secreted. Accumulated in the
CC       inter-territorial matrix of cartilage (By similarity).
CC   -!- PTM: After cleavage, the post-translationally modified ChM-I is
CC       secreted as a glycoprotein (By similarity).
CC   -!- SIMILARITY: Belongs to the chondromodulin-I family.
CC   -!- SIMILARITY: Contains 1 BRICHOS domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U43509; AAD00027.1; -.
DR   EMBL; AK013975; BAB29095.1; -.
DR   MGD; MGI:1341171; Lect1.
DR   InterPro; IPR007084; BRICHOS.
DR   Pfam; PF04089; BRICHOS; 1.
DR   PROSITE; PS50869; BRICHOS; 1.
KW   Glycoprotein; Transmembrane; Cleavage on pair of basic residues;
KW   Chondrogenesis.
FT   CHAIN         1    210       CHONDROSURFACTANT PROTEIN
FT                                (BY SIMILARITY).
FT   PROPEP      211    214       BY SIMILARITY.
FT   CHAIN       215    334       CHONDROMODULIN-I (BY SIMILARITY).
FT   TRANSMEM     46     66       POTENTIAL.
FT   DOMAIN      105    201       BRICHOS.
FT   DISULFID    282    286       BY SIMILARITY.
FT   DISULFID    283    323       BY SIMILARITY.
FT   CARBOHYD    243    243       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    108    109       AK -> RE (IN REF. 2).
FT   CONFLICT    163    163       V -> A (IN REF. 2).
FT   CONFLICT    207    207       K -> KANFA (IN REF. 2).
SQ   SEQUENCE   334 AA;  37252 MW;  DAFDEC43C7D745D6 CRC64;

  Query Match           29.7%;  Score 518;  DB 1;  Length 334;
  Best Local Similarity  36.3%;  Pred. No. 6.4e-32;
  Matches  119;  Conservative   65;  Mismatches  120;  Indels   24;  Gaps   11;

Qy          6 PENCEDCHILNAEAFKSKKICKS------LKICGLVFGILALTLIVLFW--GSKHFWPEV 57

Db         15 PEDVEFC---SPPAYTTVTVKPSGSPTRLLKVGAVV--LISGAVLLLFGAIGAFYFWKGN 69

Qy         58 PKKAYDMEHTFYSNGEKKKIYMEIDPVTRTEIPRSGNGTDETLEVHDFKNGYTGIYFVGL 117

Db         70 DNHIYNVHYSMSINGKLQDGSMEIDAVNNLETFKMGSGAKEAIEVNDFKNGITGIRFAGG 129

Qy        118 QKCFIKTQIKV-IPEF-SEPEEEIDENEE--ITTTFFEQSVIWVPAEKPIENRDFLKNSK 173

Db        130 EKCYIKAQVKARIPEVGTVTKQSISELEGKIMPVNYEENSLIWVAVDQPVKDSSFL-SSK 188

Qy        174 ILEICDNVTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTR 233

Db        189 ILELCGDLPIFWLKP--MYPKEIQRERREVVRNSAPSTTRRPHSEPRGNAGPGRLSNGTR 246

Qy        234 -HARQASEEELPINDYTE---NGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPY 289

Db        247 PNVQDDAEPFNPDNPYHQQEGESMTFDPRLDHEGICCIECRRSYTHCQKICEPLGGYYPW 306

Qy        290 PYCYQGGRVICRVIMPCNWWVARMLGRV 317

Db        307 PYNYQGCRSACRVVMPCSWWVARILGMV 334


RESULT 7
CHM1_HUMAN
ID   CHM1_HUMAN     STANDARD;      PRT;   334 AA.
AC   O75829; Q9UM18;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Chondromodulin-I precursor (ChM-I) (Leukocyte cell-derived chemotaxin
DE   1) [Contains: Chondrosurfactant protein (CH-SP)].
GN   LECT1 OR CHMI.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Chondrosarcoma;
RX   MEDLINE=98401184; PubMed=9731231;
RA   Shukunami C., Hiraki Y.;
RT   "Expression of cartilage-specific functional matrix chondromodulin-I
```

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RT   mRNA in rabbit growth plate chondrocytes and its responsiveness to
RT   growth stimuli in Vitro.";
RL   Biochem. Biophys. Res. Commun. 249:885-890(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Chondrosarcoma;
RX   MEDLINE=99203485; PubMed=10103018;
RA   Hiraki Y., Mitsui K., Endo N., Takahashi K., Hayami T., Inoue H.,
RA   Shukunami C., Tokunaga K., Kono T., Yamada M., Takahashi H.E.,
RA   Kondo J.;
RT   "Molecular cloning of human chondromodulin-I, a cartilage-derived
RT   growth modulating factor, and its expression in Chinese hamster ovary
RT   cells.";
RL   Eur. J. Biochem. 260:869-878(1999).
RN   [3]
RP   SEQUENCE OF 1-20 FROM N.A.
RA   Ozono K.;
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 215-334 FROM N.A.
RX   MEDLINE=20035732; PubMed=10570955;
RA   Hayami T., Shukunami C., Mitsui K., Endo N., Tokunaga K., Kondo J.,
RA   Takahashi H.E., Hiraki Y.;
RT   "Specific loss of chondromodulin-I gene expression in chondrosarcoma
RT   and the suppression of tumor angiogenesis and growth by its
RT   recombinant protein in vivo.";
RL   FEBS Lett. 458:436-440(1999).
RN   [5]
RP   REVIEW.
RX   MEDLINE=20367654; PubMed=10912526;
RA   Hiraki Y., Shukunami C.;
RT   "Chondromodulin-I as a novel cartilage-specific growth-modulating
RT   factor.";
RL   Pediatr. Nephrol. 14:602-605(2000).
CC   -!- FUNCTION: Bifunctional growth regulator that stimulates the growth
CC       of cultured chondrocytes in the presence of basic fibroblast
CC       growth factor (FGF) but inhibits the growth of cultured vascular
CC       endothelial cells. May contribute to the rapid growth of cartilage
CC       and vascular invasion prior to the replacement of cartilage by
CC       bone during endochondral bone development.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and secreted. Accumulated in the
CC       inter-territorial matrix of cartilage.
CC   -!- TISSUE SPECIFICITY: Cartilage specific. Weakly expressed in
CC       chondrosarcoma.
CC   -!- DEVELOPMENTAL STAGE: Expressed at 9 weeks in developing
CC       cartilagenous bone rudiments.
CC   -!- PTM: After cleavage, the post-translationally modified ChM-I is
CC       secreted as a glycoprotein.
CC   -!- SIMILARITY: Belongs to the chondromodulin-I family.
CC   -!- SIMILARITY: Contains 1 BRICHOS domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB006000; BAA33443.1; -.
DR   EMBL; AF050147; AAC98971.1; -.
DR   EMBL; AB021290; BAA77384.1; -.
DR   EMBL; AB005999; BAA86262.1; -.
DR   Genew; HGNC:17005; LECT1.
DR   MIM; 605147; -.
DR   GO; GO:0008151; P:cell growth and/or maintenance; TAS.
DR   GO; GO:0006029; P:proteoglycan metabolism; TAS.
DR   GO; GO:0001501; P:skeletal development; TAS.
DR   InterPro; IPR007084; BRICHOS.
DR   Pfam; PF04089; BRICHOS; 1.
DR   PROSITE; PS50869; BRICHOS; 1.
KW   Glycoprotein; Transmembrane; Cleavage on pair of basic residues;
KW   Chondrogenesis.
FT   CHAIN         1    210       CHONDROSURFACTANT PROTEIN
FT                                (BY SIMILARITY).
FT   PROPEP      211    214       POTENTIAL.
FT   CHAIN       215    334       CHONDROMODULIN-I.
FT   TRANSMEM     45     65       POTENTIAL.
FT   DOMAIN      104    201       BRICHOS.
FT   DISULFID    282    286       BY SIMILARITY.
FT   DISULFID    283    323       BY SIMILARITY.
FT   CARBOHYD    243    243       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   334 AA;  37102 MW;  9E2393111F9D4FE5 CRC64;

  Query Match             29.6%;  Score 516;  DB 1;  Length 334;
  Best Local Similarity   35.2%;  Pred. No. 9.1e-32;
  Matches  118;  Conservative   63;  Mismatches  116;  Indels   38;  Gaps   12;

Qy          6 PENCEDCHILNAEAF-----KSKKICKSLKICGLVFGILALTLIVLFW--GSKHFWPEVP 58
              |:: | |  :  |:     |     : ||:  :|  :::  :::||   |: :||
Db         15 PDDVEFC---SPPAYATLTVKPSSPARLLKVGAVV--LISGAVLLLFGAIGAFYFWKGSD 69

Qy         59 KKAYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQ 118
                |:: :|   ||: :   ||||      | |: |:| :| : |:||:|| ||| | | :
Db         70 SHIYNVHYTMSINGKLQDGSMEIDAGNNLETFKMGSGAEEAIAVNDFQNGITGIRFAGGE 129

Qy        119 KCFIKTQIKV-IPEF-SEPEEEID---ENEEITTTFFEQSVIWVPAEKPIENRDFLKNSK 173
             ||:|| |:|  |||  :  :: |    | : :   : | |:|||  ::|::: || :||
Db        130 KCYIKAQVKARIPEVGAVTKQSISSKLEGKIMPVKYEENSLIWVAVDQPVKDNSFL-SSK 188

Qy        174 ILEICDNVTMYWINPTLISVSELQDFEEEGEDLHFPANEKK----------GIEQNEQW 222
             :||:| :: ::|: ||     |:|    |    |   |:          |   ||
Db        189 VLELCGDLPIFWLKPTY--PKEIQRERREVVRKIVPTTTKRPHSGPRSNPGAGRLNNE-- 244

Qy        223 VVPQVKVEKTRHARQASEEELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEP 282
               | |: :      ||   : | :      : ||| ||  | ||| |||   :|:::|||
Db        245 TRPSVQEDS-----QAFNPDNPYHQQEGESMTFDPRLDHEGICCIECRRSYTHCQKICEP 299

Qy        283 LLGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV 317
              | ||||:|| ||| |  |||||||:|||||:|| |
Db        300 LGGYYPWPYNYQGCRSACRVIMPCSWWVARILGMV 334


RESULT 8
CHM1_BOVIN
ID   CHM1_BOVIN     STANDARD;      PRT;   335 AA.
AC   P17404; P23590;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Chondromodulin-I precursor (ChM-I) (Leukocyte cell-derived chemotaxin
DE   1) (Small cartilage-derived glycoprotein) (SCGP) [Contains:
DE   Chondrosurfactant protein (CH-SP)].
GN   LECT1 OR CHM1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 215-241 AND 297-317.
RC   TISSUE=Fetal epiphyseal cartilage;
RX   MEDLINE=91222210; PubMed=1709014;
RA   Hiraki Y., Tanaka H., Inoue H., Kondo J., Kamizono A., Suzuki F.;
RT   "Molecular cloning of a new class of cartilage-specific matrix,
RT   chondromodulin-I, which stimulates growth of cultured chondrocytes.";
RL   Biochem. Biophys. Res. Commun. 175:971-977(1991).
RN   [2]
RP   SEQUENCE OF 215-335, VARIANT MET-221, AND GLYCOSYLATION.
RC   TISSUE=Nasal cartilage;
RX   MEDLINE=90277643; PubMed=2351661;
RA   Neame P.J., Treep J.T., Young C.N.;
RT   "An 18-kDa glycoprotein from bovine nasal cartilage. Isolation and
RT   primary structure of small, cartilage-derived glycoprotein.";
RL   J. Biol. Chem. 265:9628-9633(1990).
RN   [3]
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RP   ERRATUM.
RA   Neame P.J., Treep J.T., Young C.N.;
RL   J. Biol. Chem. 265:22056-22056(1990).
RN   [4]
RP   PROCESSING.
RX   MEDLINE=21316541; PubMed=11323410;
RA   Azizan A., Holaday N., Neame P.J.;
RT   "Post-translational processing of bovine chondromodulin-I.";
RL   J. Biol. Chem. 276:23632-23638(2001).
RN   [5]
RP   REVIEW.
RX   MEDLINE=20367654; PubMed=10912526;
RA   Hiraki Y., Shukunami C.;
RT   "Chondromodulin-I as a novel cartilage-specific growth-modulating
RT   factor.";
RL   Pediatr. Nephrol. 14:602-605(2000).
CC   -!- FUNCTION: Bifunctional growth regulator that stimulates the growth
CC       of cultured chondrocytes in the presence of basic fibroblast
CC       growth factor (FGF) but inhibits the growth of cultured vascular
CC       endothelial cells. May contribute to the rapid growth of cartilage
CC       and vascular invasion prior to the replacement of cartilage by
CC       bone during endochondral bone development.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and secreted. Accumulated in the
CC       inter-territorial matrix of cartilage.
CC   -!- TISSUE SPECIFICITY: Nasal and articular cartilage, and fetal
CC       epiphysis.
CC   -!- PTM: After cleavage, the post-translationally modified ChM-I is
CC       secreted as a glycoprotein.
CC   -!- PTM: Two other smaller nonglycosylated chondromodulin forms (9 kDa
CC       and 7kDa) are found either in developing articular cartilage or in
CC       chondrocytes. The 9 kDa form could be processed by an
CC       extracellular matrix-associated protease as a metalloproteinase
CC       and the 7 kDa form could be processed intracellularly.
CC   -!- SIMILARITY: Belongs to the chondromodulin-I family.
CC   -!- SIMILARITY: Contains 1 BRICHOS domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M65081; AAA30445.1; -.
DR   PIR; JT0569; JT0569.
DR   InterPro; IPR007084; BRICHOS.
DR   Pfam; PF04089; BRICHOS; 1.
DR   PROSITE; PS50869; BRICHOS; 1.
KW   Glycoprotein; Transmembrane; Cleavage on pair of basic residues;
KW   Chondrogenesis.
FT   CHAIN         1    210       CHONDROSURFACTANT PROTEIN (POTENTIAL).
FT   PROPEP      211    214       POTENTIAL.
FT   CHAIN       215    335       CHONDROMODULIN-I.
FT   TRANSMEM     45     65       POTENTIAL.
FT   DOMAIN      104    201       BRICHOS.
FT   DISULFID    283    287
FT   DISULFID    284    324
FT   CARBOHYD    223    223       O-LINKED.
FT   CARBOHYD    236    236       O-LINKED (GALNAC. . .).
FT   CARBOHYD    244    244       N-LINKED (GLCNAC. . .).
FT   VARIANT     221    221       V -> M.
FT   CONFLICT    223    224       TT -> NE (IN REF. 2).
FT   CONFLICT    256    256       P -> PD (IN REF. 2).
SQ   SEQUENCE   335 AA;  37164 MW;  6D72CA8740448441 CRC64;

  Query Match             29.5%;  Score 514.5;  DB 1;  Length 335;
  Best Local Similarity   33.0%;  Pred. No. 1.2e-31;
  Matches  115;  Conservative   60;  Mismatches  109;  Indels   65;  Gaps    8;

Qy          6 PENCEDCH--ILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKKAYD 63
              |:: | |       |   |     : ||:  :|    |: |::   |: :||       |:
Db         15 PDDVEFCSPPAYAAVTVKPSSPARLLKVGAVVLISGAVLLLLGAIGAFYFWKGSDNHIYN 74

Qy         64 MEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIK 123
              : :|   ||: :   ||||     | |: |:| :| :||:||:|| ||| | | :||:||
Db         75 VHYTMSINGKLQDGSMEIDAGNNLETFKMGSGAEEAVEVNDPQNGITGIRFAGGEKCYIK 134

Qy        124 TQIKV-IPEF---------SEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSK 173
               |:|  |||           || | :|     :   : | |:||  ::|:::  || :||
Db        135 AQVKARIPEVGTMTKQSISSELEGKI-----MPVKYEENSLIWVAGDQPVKDNSFL-SSK 188

Qy        174 ILEICDNVTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTR 233
              :||:| :: ::|: ||                 :|    | |::  : :| ::     |
Db        189 VLELCGDLPIFWLKPT-----------------YP----KEIQRERRELVRKIVTTTTT 226

Qy        234 HARQASEEELPINDYTENG------------------------IEFDPMLDERGYCCIY 268
                 ::  :  |      ||                       : ||| ||  | |||
Db        227 RRLRSGPQGTPAPGRPNNGTRPSVQEDAEPFNPDNPYHQQEGESMTFDPRLDHEGICCIE 286

Qy        269 CRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV 317
              |||   :|:::|||| ||:|:|| ||| |  |||||||:|||||:|| |
Db        287 CRRSYTHCQKICEPLGGYHPWPYNYQGCRSACRVIMPCSWWVARILGMV 335


RESULT 9
CHM1_RABIT
ID   CHM1_RABIT     STANDARD;      PRT;   333 AA.
AC   O77770;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Chondromodulin-I precursor (ChM-I) (Leukocyte cell-derived chemotaxin
DE   1) [Contains: Chondrosurfactant protein (CH-SP)].
GN   LECT1 OR CHM1.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98401184; PubMed=9731231;
RA   Shukunami C., Hiraki Y.;
RT   "Expression of cartilage-specific functional matrix chondromodulin-I
RT   mRNA in rabbit growth plate chondrocytes and its responsiveness to
RT   growth stimuli in Vitro.";
RL   Biochem. Biophys. Res. Commun. 249:885-890(1998).
RN   [2]
RP   REVIEW.
RX   MEDLINE=20367654; PubMed=10912526;
RA   Hiraki Y., Shukunami C.;
RT   "Chondromodulin-I as a novel cartilage-specific growth-modulating
RT   factor.";
RL   Pediatr. Nephrol. 14:602-605(2000).
CC   -!- FUNCTION: Bifunctional growth regulator that stimulates the growth
CC       of cultured chondrocytes in the presence of basic fibroblast
CC       growth factor (FGF) but inhibits the growth of cultured vascular
CC       endothelial cells. May contribute to the rapid growth of cartilage
CC       and vascular invasion prior to the replacement of cartilage by
CC       bone during endochondral bone development (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and secreted. Accumulated in the
CC       inter-territorial matrix of cartilage (By similarity).
CC   -!- PTM: After cleavage, the post-translationally modified ChM-I is
CC       secreted as a glycoprotein (By similarity).
CC   -!- SIMILARITY: Belongs to the chondromodulin-I family.
CC   -!- SIMILARITY: Contains 1 BRICHOS domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF072129; AAC36470.1; -.
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DR   InterPro; IPR007084; BRICHOS.
DR   Pfam; PF04089; BRICHOS; 1.
DR   PROSITE; PS50869; BRICHOS; 1.
KW   Glycoprotein; Transmembrane; Cleavage on pair of basic residues;
KW   Chondrogenesis.
FT   CHAIN         1    210       CHONDROSURFACTANT PROTEIN
FT                                (BY SIMILARITY).
FT   PROPEP      211    214       POTENTIAL.
FT   CHAIN       215    333       CHONDROMODULIN-I.
FT   TRANSMEM     42     62       POTENTIAL.
FT   DOMAIN      104    201       BRICHOS.
FT   DISULFID    281    285       BY SIMILARITY.
FT   DISULFID    282    322       BY SIMILARITY.
FT   CARBOHYD    243    243       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   333 AA;  36974 MW;  70B5FFA9613DEA1D CRC64;

  Query Match             28.2%;  Score 492.5;  DB 1;  Length 333;
  Best Local Similarity   33.4%;  Pred. No. 5.3e-30;
  Matches  110;  Conservative   72;  Mismatches  120;  Indels   27;  Gaps   12;

Qy          6 PENCEDCHILNAEAFKSKKI-----CKSLKICGLVFGILALTLIVLFW--GSKHFWPEVP 58
              |:: | |      |: :  :      : ||:  :|  :::  :::||   |: : |
Db         15 PDDVEFC---GPPAYATVTVKPSGPARLLKVGAVV--LISGAVLLLFGAIGAFYLWKGSD 69

Qy         59 KKAYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQ 118
                |:: :|   ||: :   ||||      | |: |:| :| :||:||:|| ||| | | :
Db         70 NHIYNVHYTMSINGKLQDGSMEIDARNNLETFKMGSGAEEAIEVNDFQNGITGIRFAGGE 129

Qy        119 KCFIKTQIKV-IPEF-SEPEEEID---ENEEITTTFFEQSVIWVPAEKPIENRDFLKNSK 173
              ||:|| |:|  :||  :  :: |    | : :     |:::|||   :|:::  || :::
Db        130 KCYIKAQVKARVPEVGTVTQQSISSELEGKIMPVKHEEEALVWVAVGQPVQDNSFL-SAR 188

Qy        174 ILEICDNVTMYWINPTLISVSELQDFEEEGEDLHFPANEKK---GIEQNEQWVVPQVKVE 230
              :||:| :: ::|: ||      |:|     |      |  |:   |   |        ::: :
Db        189 VLELCGDLPIFWLKPTY--PKEIQRERREVVRKTVPTTTKRPHSGPRGNPG--PARMRND 244

Qy        231 KTRHARQASEEELPINDYTENG--IEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP 288
              :: ||   | | | : |  : ||| ||  | ||| |||   :|:::|||| || |
Db        245 SRPSVQEDSEPFNPDNPYHQEGESMTFDPRLDHEGICCIECRRSYTHCQKICEPLGGYNP 304

Qy        289 YPYCYQGGRVICRVIMPCNWWVARMLGRV 317
              :|| ||| |  |||:|||:|||||:|| |
Db        305 WPYNYQGCRSACRVVMPCSWWVARILGMV 333


RESULT 10
CHM1_BRARE
ID   CHM1_BRARE     STANDARD;      PRT;   286 AA.
AC   P58239;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Chondromodulin-I precursor (ChM-I) (Leukocyte cell-derived chemotaxin
DE   1) [Contains: Chondrosurfactant protein (CH-SP)].
GN   LECT1 OR CHM1 OR CHMI.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21322690; PubMed=11429291;
RA   Sachdev S.W., Dietz U.H., Oshima Y., Lang M.R., Knapik E.W.,
RA   Hiraki Y., Shukunami C.;
RT   "Sequence analysis of zebrafish chondromodulin-1 and expression
RT   profile in the notochord and chondrogenic regions during cartilage
RT   morphogenesis.";
RL   Mech. Dev. 105:157-162(2001).
CC   -!- FUNCTION: Bifunctional growth regulator. May contribute to the
CC       rapid growth of cartilage and vascular invasion prior to the
CC       replacement of cartilage by bone during endochondral bone
CC       development (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and secreted. Accumulated in the
CC       inter-territorial matrix of cartilage (By similarity).
CC   -!- PTM: After cleavage, the post-translationally modified ChM-I is
CC       secreted as a glycoprotein (By similarity).
CC   -!- SIMILARITY: Belongs to the chondromodulin-I family.
CC   -!- SIMILARITY: Contains 1 BRICHOS domain.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF322374; AAK77023.1; -.
DR   ZFIN; ZDB-GENE-010713-1; lect1.
DR   InterPro; IPR007084; BRICHOS.
DR   Pfam; PF04089; BRICHOS; 1.
DR   PROSITE; PS50869; BRICHOS; 1.
KW   Glycoprotein; Transmembrane; Cleavage on pair of basic residues;
KW   Chondrogenesis.
FT   CHAIN         1    165       CHONDROSURFACTANT PROTEIN
FT                                (BY SIMILARITY).
FT   PROPEP      166    169       POTENTIAL.
FT   CHAIN       170    286       CHONDROMODULIN-I.
FT   TRANSMEM     29     49       POTENTIAL.
FT   DOMAIN       75    157       BRICHOS.
FT   DISULFID    234    238       BY SIMILARITY.
FT   DISULFID    235    275       BY SIMILARITY.
FT   CARBOHYD    191    191       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   286 AA;  32235 MW;  21B377E0348EDDB3 CRC64;

  Query Match             23.1%;  Score 403.5;  DB 1;  Length 286;
  Best Local Similarity   32.3%;  Pred. No. 2.2e-23;
  Matches  108;  Conservative   40;  Mismatches  113;  Indels   73;  Gaps   14;

Qy          7 ENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFW--GSKHFWPEVPKKAYDM 64
              |  |   :      | | : | |   : |  :|   ::||   |: : |     |:|
Db          3 ETAEKTPVEAYSTLKPKGLMKMKKTALVAF--IAGAALLLFGGVGAFYLWKVTEKEAISA 60

Qy         65 EHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKT 124
                  |   | :| |          |  ||   :|| ||| | | : | | :|||||:
Db         61 H-----LGRNIDIKIENDS-------DSAEGT--IVEVQDFKAGITAVKFPGKEKCFIKS 106

Qy        125 QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDNVTMY 184
              | :   | || |  :    |:       |::|: :|:|:::  || : :||  | :: :|
Db        107 QART--ELSEDEAGV--KAEVA------SLVWITSEEPLKDSSFL-SPEILRFCADLPIY 155

Qy        185 WINPTLISVSELQDFEEEGEDLHFPANEK---------------KGIEQNEQWVVPQVK 228
              |                     | ||| :               |:  | |    :
Db        156 W---------------------HHPANSRALRKRRSATRMRRQTSAGV--NRQPARRRNS 192

Qy        229 VEKTRHARQASEEELPINDYTEN-GIE----FDPMLDERGYCCIYCRRGNRYCRRVCEPL 283
                |   |    |  | | | :| | |    |||||| || ||  | |   :| ||||||
Db        193 TASARDERPTGPEYNPENPYHQNQGSEGTMVFDPMLDHRGICCTECHRSYTHCERVCEPL 252

Qy        284 LGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV 317
                ||:|:|| | | | :||:|||| || ||:|| |
Db        253 GGYWPWPYNYHGCRPVCRLIMPCRWWAARVLGLV 286


RESULT 11
SPB8_HUMAN
ID   SPB8_HUMAN     STANDARD;      PRT;   374 AA.
AC   P50452;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Cytoplasmic antiproteinase 2 (CAP2) (CAP-2) (Protease inhibitor 8)
DE   (Serpin B8).
GN   SERPINB8 OR PI8.
OS   Homo sapiens (Human).
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=96102039; PubMed=8530382;
RA   Sprecher C.A., Morgenstern K.A., Mathewes S., Dahlen J.R.,
RA   Schrader S.K., Foster D.C., Kisiel W.;
RT   "Molecular cloning, expression, and partial characterization of two
RT   novel members of the ovalbumin family of serine proteinase
RT   inhibitors.";
RL   J. Biol. Chem. 270:29854-29861(1995).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: Belongs to the serpin family. Ov-serpin subfamily.
CC   -----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; L40377; AAC41939.1; -.
DR   PIR; A59273; A59273.
DR   HSSP; P05120; 1BY7.
DR   Genew; HGNC:8952; SERPINB8.
DR   MIM; 601697; -.
DR   GO; GO:0005829; C:cytosol; TAS.
DR   GO; GO:0005515; F:protein binding; TAS.
DR   GO; GO:0004868; F:serpin; TAS.
DR   InterPro; IPR000215; Serpin.
DR   Pfam; PF00079; serpin; 1.
DR   SMART; SM00093; SERPIN; 1.
DR   PROSITE; PS00284; SERPIN; 1.
KW   Serpin; Serine protease inhibitor.
FT   ACT_SITE    339    340       REACTIVE BOND (BY SIMILARITY).
SQ   SEQUENCE   374 AA;  42786 MW;  E855A033519AC60E CRC64;

  Query Match             5.6%;  Score 97.5;  DB 1;  Length 374;
  Best Local Similarity   21.3%;  Pred. No. 3.6;
  Matches   63;  Conservative   42;  Mismatches  112;  Indels   79;  Gaps   14;

Qy          7 ENCEDC--HILNAEAFKSKKICKSLKICGLVFGILALTLI--VLFWGSKHFWPEVPKKAY 62
              |: |:|  || :  | |::    :  | |  :  | |:  : | |   | |   : |
Db        123 EDTEECRKHINDWVAEKTEGKISEVLDAGTVDPLTKLVLVNAIYFKGK---WNEQFDRKY 179

Qy         63 DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFI 122
                 | :| ||| : |         :|:             || ||           :
Db        180 TRGMLFKTNEEKKTVQM---------MFKEAK----------FKMGYAD---------EV 211

Qy        123 KTQIKVIPEFSEPEEEI-------DENEEITTT---FFEQSVIWVPAEKPIENR--DFL 169
                ||:  :|     |||:       :|| ::       :|:   |  :||  :::   ||
Db        212 HTQVLELPYV---EEELSMVILLPDDNTDLAVVEKALTYEKFKAWTNSEKLTKSKVQVFL 268

Qy        170 KNSKILEICDNVTMYWINPTLISVSELQDFEEEGEDLHFPANEKK----------GIEQN 219
                |: |      | :|  |    : ||           :| |
Db        269 PRLKLEE------SYDLEPFLRRLGMIDAFDEAKADFSGMSTEKNVPLSKVAHKCFVEVN 322

Qy        220 EQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPML----DERGYCCIYCRR 271
              |:          |::| :  |     |:         :  | ::| |
Db        323 EEGTEAAAATAVVRNSRCSRMEPRFCADH--------PFLFFIRRHKTNCILFCGR 370


RESULT 12
YKDA_MYCCA
ID   YKDA_MYCCA     STANDARD;      PRT;   655 AA.
AC   P45615;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Hypothetical lipoprotein in kdtB 5'region precursor (ORFA).
OS   Mycoplasma capricolum.
OC   Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX   NCBI_TaxID=2095;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 27343 / Kid;
RX   MEDLINE=95218642; PubMed=7703858;
RA   Zhu P.-P., Reizer J., Peterkofsky A.;
RT   "Unique dicistronic operon (ptsI-crr) in Mycoplasma capricolum
RT   encoding enzyme I and the glucose-specific enzyme IIA of the
RT   phosphoenolpyruvate:sugar phosphotransferase system: cloning,
RT   sequencing, promoter analysis, and protein characterization.";
RL   Protein Sci. 3:2115-2128(1994).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC       (Potential).
CC   -!- SIMILARITY: BELONGS TO THE MG067 / MG068 / MG395 FAMILY.
CC   -----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; U15110; AAA70404.1; -.
DR   PIR; A57681; A57681.
DR   InterPro; IPR002414; DUF30/31.
DR   InterPro; IPR000437; Prok_lipoprot_S.
DR   Pfam; PF01732; DUF31; 1.
DR   PRINTS; PR00840; Y06768FAMILY.
DR   PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW   Hypothetical protein; Lipoprotein; Membrane; Signal; Palmitate.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    655       HYPOTHETICAL LIPOPROTEIN IN KDTB
FT                                5'REGION.
FT   LIPID        24     24       N-palmitoyl cysteine (Potential).
FT   LIPID        24     24       S-diacylglycerol cysteine (Potential).
SQ   SEQUENCE   655 AA;  75908 MW;  AD3E4B0EA0D7B060 CRC64;

  Query Match             5.6%;  Score 97;  DB 1;  Length 655;
  Best Local Similarity   21.3%;  Pred. No. 7.8;
  Matches   57;  Conservative   44;  Mismatches   99;  Indels   68;  Gaps   12;

Qy          7 ENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKKAYDMEH 66
              :| ||      |  :|| |                              ::| :|:  |
Db        155 DNIEDIDDSKLEILESKYI----------------------PNQHNYPDYVKN------ 185

Qy         67 TFYSNGEKKKIYMEIDPVTRT----------EIFRSGNGTDETLEVHDFKNGYTGIYFVG 116
               :     ::|| |:    | :          :  :| ||    |: | : |  | | |
Db        186 --FKTVSAEEIYKELYDRTFSIKFLVKLKDGGLLSNGTGTGWLLDYHKYSN--TNKY--- 238

Qy        117 LQKCFIKTQIKVIPEFSEPEEEIDENEEITTTFFEQS---VIWVPAEKPIENRDFLKNSK 173
                | || | : |: :||     : ::|:|    ::: |    || :    |      || : :
Db        239 --KMFIATNLHVLADFSNSLTD-EQNKEF--NYYDPSGNKVIGLGLGKADNVTDFSRKNN 293

Qy        174 ILEICDNVTMYWINPTLISVSELQDFEEEGEDLHFPANE-KKGIEQNEQWVVPQVKVEKT 232
                :  :|:  |::|          ||||   ::  :  |:  |||  :  : |    |
Db        294 NSKSENNIANYYLNN--------QDFENYLKNDFWSVNKFSKGISE-PKIVFGAVDFMKD 344

Qy        233 R----HARQASEEELPINDYTENGIEFD 256
              |    |     :| :   :| :|  | :
Db        345 RAIKNHYEALQKEAINYYNYKKNNNEIN 372


RESULT 13
RRPL_VSVJO
ID   RRPL_VSVJO     STANDARD;      PRT;  2109 AA.
AC   P16379;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
```

```
DE   (L protein).
GN   L.
OS   Vesicular stomatitis virus (serotype New Jersey / strain Ogden).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Rhabdoviridae; Vesiculovirus.
OX   NCBI_TaxID=11283;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90177235; PubMed=2155516;
RA   Barik S., Rud E.W., Luk D., Banerjee A.K., Kang C.Y.;
RT   "Nucleotide sequence analysis of the L gene of vesicular stomatitis
RT   virus (New Jersey serotype): identification of conserved domains in L
RT   proteins of nonsegmented negative-strand RNA viruses.";
RL   Virology 175:332-337(1990).
CC   -!- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
CC       POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPPING, AS WELL AS
CC       METHYLATION OF CAPS, AND POLY(A) SYNTHESIS.
CC   -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC       {RNA}(N).
CC   -!- SUBUNIT: THOUGHT TO FORM A TRANSCRIPTION COMPLEX WITH THE
CC       NUCLEOCAPSID (N) PROTEIN.
CC   -!- SIMILARITY: WITH THE L PROTEIN OF OTHER RHABDOVIRUSES AND
CC       PARAMYXOVIRUSES.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M29788; AAA48442.1; -.
DR   PIR; A46309; A46309.
DR   InterPro; IPR007098; RNA_pol_monon.
DR   InterPro; IPR002877; RrmJ_FtsJ.
DR   InterPro; IPR001016; Viral_RNA_pol_L.
DR   Pfam; PF01728; FtsJ; 1.
DR   Pfam; PF00946; Paramyx_RNA_pol; 1.
KW   Transferase; RNA-directed RNA polymerase.
SQ   SEQUENCE   2109 AA;  242111 MW;  724CF90ECE26CAB9 CRC64;

  Query Match             5.5%;  Score 96;  DB 1;  Length 2109;
  Best Local Similarity   22.1%;  Pred. No. 39;
  Matches   52;  Conservative   46;  Mismatches   91;  Indels   46;  Gaps   13;

Qy         55 PEVPKKAYDMEHTFYSNGEKKKIYMEIDPV-TRTEIFRSGNGTDETLEVH-DFKN-GYTG 111
              |::||  :  ||      |  :::    : : |  ::  |     |  | |:  |:: |:
Db        306 PKIPKFPHFEEHV---KGSVQELTQRSNRIQTLYDLIMSMKDVDLVLVVYGSPRHWGHPF 362

Qy        112 I-YFVGLQKCFIKTQIKVIPEFSEPEEEIDEN--EEITTTF--------FEQSVIWV--- 157
              | || ||:|  : ||: :        |: ||:  ::: :          | :|  |
Db        363 IDYFQGLEK--LHTQVNM-------EKHIDKEYPQQLASDLARLVLNKQFSESKKWFVDP 413

Qy        158 -------PAEKPIENRDFLKNSKILEICDNVTMYWINPTLISVSELQDFEEEG---EDLH 207
                    |  : : |: :   :|| :  ||    |    ||   |: |  :       |
Db        414 SKMSPKHPFYEHVINKTWPTAAKIQDFGDN----WHKLPLIQCFEIPDLIDPSVIYSDKS 469

Qy        208 FPANEKKGIE---QNEQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPML 259
                |:|: |:         :|  || :|    :|:  :  : |  |||:: | ::
Db        470 HSMNKKEVIQHVRSKPNIPIPSNKVLQTMLTNRATNWKAFLKDIDENGLDDDDLI 524


RESULT 14
YF54_METJA
ID   YF54_METJA     STANDARD;      PRT;   622 AA.
AC   Q58949;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical protein MJ1554 precursor.
GN   MJ1554.
OS   Methanococcus jannaschii.
OC   Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC   Methanocaldococcaceae; Methanocaldococcus.
OX   NCBI_TaxID=2190;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX   MEDLINE=96337999; PubMed=8688087;
RA   Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA   Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA   Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA   Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA   Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA   Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA   Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA   Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT   "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT   jannaschii.";
RL   Science 273:1058-1073(1996).
CC   -!- SIMILARITY: TO A.FULGIDUS AF0817.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U67596; AAB99574.1; -.
DR   PIR; A64494; A64494.
DR   TIGR; MJ1554; -.
DR   InterPro; IPR000437; Prok_lipoprot_S.
KW   Hypothetical protein; Signal; Complete proteome.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    622       HYPOTHETICAL PROTEIN MJ1554.
SQ   SEQUENCE   622 AA;  72282 MW;  86CAA62F3854D73F CRC64;

  Query Match             5.5%;  Score 95.5;  DB 1;  Length 622;
  Best Local Similarity   22.0%;  Pred. No. 9.4;
  Matches   56;  Conservative   40;  Mismatches   79;  Indels   79;  Gaps   13;

Qy         21 KSKKICKSLKICGLVFGILALTLIVLFWGSKHFW----PEVPKKAYDMEHTFYSNGEKKK 76
              |  || |::  || :: :   ||||: |     :    ||:||  : |:     ||
Db        132 KYAKIIKNISECGYLY-LTNNTLIVISWNKITSYNVSNPEMPKIIWQMD----LNGS--- 183

Qy         77 IYMEIDPVTRTEIFRSGNGT----------DETLEVHDFKNGYTGIYF------------ 114
               |::          |  |||          |  :  :::| ||   |
Db        184 -YVD---------SRLYNGTLYLVVRKNSIDCPIVWNNYKIGYDKYYIPELPPIYSMDFD 233

Qy        115 -------VGLQKCFIKTQIKVIPEFSEP------------EEEIDENEEITTTFFEQSVI 155
                  : ::   ::  | ::  :                      :|:| : :      | :
Db        234 TTYIISRINIKSGKVENSIAIVGNYKTTLYMSKNNLYFAYNLKINEKKLMLNFLNESADK 293

Qy        156 WVPAE------KPIENRDFLKNSKILEICDNVTMYWINPTLIS------VSELQ-DFEEE 202
              : | |      : ||| ||  |:| :|| : :  |    :| |      : :|| |||
Db        294 YFPTEVADKIKRVIENEDFGDNAKFVEITETIERYL--SSLPSEKRHNLMKKLQNDFENY 351

Qy        203 GEDLHFPANEKKGI 216
              |: |:   |  ||
Db        352 LEE-HWEEFEYTGI 364


RESULT 15
SPR2_CAEEL
ID   SPR2_CAEEL     STANDARD;      PRT;   312 AA.
AC   Q18240; Q9GPJ0;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Suppressor of presenilin 2.
GN   SPR-2 OR C27B7.1.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
```

```
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
RP   SPECIFICITY.
RC   STRAIN=Bristol N2;
RX   MEDLINE=20570513; PubMed=11114162;
RA   Wen C., Levitan D., Li X., Greenwald I.;
RT   "spr-2, a suppressor of the egg-laying defect caused by loss of sel-12
RT   presenilin in Caenorhabditis elegans, is a member of the SET protein
RT   subfamily.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:14524-14529(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Matthews P.;
RL   Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   REVISIONS.
RA   Durbin R.;
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Potential corepressor protein, which may affect
CC       chromatin structure and/or transcription. May participate in the
CC       transcriptional repression of the presenilin protein hop-1.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- TISSUE SPECIFICITY: Widely expressed.
CC   -!- MISCELLANEOUS: Loss of function results in a suppression of sel-12
CC       mutant phenotypes, possibly by upregulating hop-1 expression.
CC   -!- SIMILARITY: Belongs to the nucleosome assembly protein (NAP)
CC       family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF321546; AAG42102.1; -.
DR   EMBL; Z54236; CAA90979.2; -.
DR   WormPep; C27B7.1; CE27804.
DR   InterPro; IPR002164; NAP_family.
DR   Pfam; PF00956; NAP; 1.
KW   Transcription regulation; Repressor; Nuclear protein.
FT   DOMAIN      214    300       GLU-RICH.
SQ   SEQUENCE   312 AA;  35874 MW;  0CB087474841A1DC CRC64;

  Query Match             5.4%;  Score 95;  DB 1;  Length 312;
  Best Local Similarity   22.4%;  Pred. No. 4.4;
  Matches   47;  Conservative   38;  Mismatches   55;  Indels   70;  Gaps   12;

Qy        100 LEVHDFKNGYTGIYFVGLQKCFIKTQIKVIPEFSEPEEEIDENEEITTTFFEQS------ 153
              ||| :|:::               :::  |:|  | :| |    || || ::  ||
Db        109 LEVQEFED-------------LRSGFKIIMTF-DPNEYF-TNEVITKSYHLQSESPSTE 152

Qy        154 ---VIWVPAEKPIENRD------FLK---------NSKILEICD-----NVTMYWINPTL 190
                  : |   :||    |       ||:         : :| |:       |   |:: |
Db        153 ITEIEWKENKKPPFPEDGDSAHTFLEWLTYAALPDSDEIAEVIKDDLYVNPLQYYVMP-- 210

Qy        191 ISVSELQDFEEEGEDLHFPANEKKGIEQNEQW-----VVPQVKVEKTRHA---RQASEEE 242
                ::|: ||  :|:    ||::|:::| |      :   :||::   |       |||
Db        211 ----DMQEVEE--DDIEDFLNEERGVDENGQRIPRRNISDSLKVDQDESADGQEGEDEEE 264

Qy        243 LPINDYTENGI---------EFDPMLDERG 263
                : :  |:|:         | |  ::| |
Db        265 EDMGEEEEDGVEEEAEGEEEEEDGAIEEEG 294


Search completed: March 30, 2004, 14:31:33
Job time : 19 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2004, 14:29:47 ; Search time 45 Seconds
(without alignments)
2222.650 Million cell updates/sec

Title: US-10-089-600-2
Perfect score: 1745
Sequence: 1 MAKNPPENCEDCHILNAEAF.....VICRVIMPCNWWVARMLGRV 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1709	97.9	317	6	Q95M14	Q95m14 equus cabal
2	741	42.5	135	11	Q8CET4	Q8cet4 mus musculu
3	545	31.2	338	13	Q7ZY92	Q7zy92 xenopus lae
4	521	29.9	334	11	Q80UX1	Q80ux1 mus musculu
5	518.5	29.7	333	4	Q8TAY6	Q8tay6 homo sapien
6	264	15.1	50	6	Q95LQ7	Q95lq7 equus cabal
7	112.5	6.4	499	16	Q97LJ5	Q97lj5 clostridium
8	108	6.2	5458	5	Q9U459	Q9u459 plasmodium
9	108	6.2	5507	5	Q8IHN3	Q8ihn3 plasmodium
10	105.5	6.0	2227	5	Q8II21	Q8ii21 plasmodium
11	104.5	6.0	494	17	Q8PUI9	Q8pui9 methanosarc
12	103.5	5.9	938	5	Q8IHY0	Q8ihy0 plasmodium
13	103	5.9	1248	5	Q8I204	Q8i204 plasmodium
14	101.5	5.8	1612	5	Q8IFN0	Q8ifn0 plasmodium
15	100.5	5.8	265	16	Q8ENF6	Q8enf6 oceanobacil
16	100.5	5.8	350	5	Q9UAY5	Q9uay5 caenorhabdi
17	100	5.7	827	16	Q98QV4	Q98qv4 mycoplasma
18	100	5.7	844	10	O04498	O04498 arabidopsis
19	99	5.7	679	5	Q8IIE0	Q8iie0 plasmodium
20	98.5	5.6	487	5	Q8MV47	Q8mv47 plasmodium
21	98.5	5.6	487	5	Q8II16	Q8ii16 plasmodium
22	98	5.6	1253	5	Q8IKA0	Q8ika0 plasmodium
23	98	5.6	2109	12	Q8B544	Q8b544 vesicular s
24	98	5.6	16215	5	Q9NFS3	Q9nfs3 drosophila
25	98	5.6	18074	5	Q9I7U4	Q9i7u4 drosophila
26	97.5	5.6	149	11	Q62810	Q62810 rattus norv
27	97.5	5.6	309	4	Q9H4K1	Q9h4k1 homo sapien
28	97.5	5.6	494	17	Q8PXB4	Q8pxb4 methanosarc
29	97.5	5.6	494	17	Q8PUY6	Q8puy6 methanosarc
30	97.5	5.6	799	16	Q9PR12	Q9pr12 ureaplasma
31	97	5.6	184	4	Q86XP6	Q86xp6 homo sapien
32	97	5.6	3901	5	Q9N533	Q9n533 caenorhabdi
33	96.5	5.5	313	11	O35531	O35531 rattus norv
34	96.5	5.5	374	4	Q7Z2V6	Q7z2v6 homo sapien
35	96.5	5.5	494	17	Q8TTG5	Q8ttg5 methanosarc
36	96.5	5.5	494	17	Q8TRX0	Q8trx0 methanosarc
37	96.5	5.5	497	17	Q8TMH9	Q8tmh9 methanosarc
38	96.5	5.5	513	17	Q8TS61	Q8ts61 methanosarc
39	96.5	5.5	732	17	P95869	P95869 sulfolobus
40	95.5	5.5	752	16	Q9CGC9	Q9cgc9 lactococcus
41	95.5	5.5	837	5	Q25751	Q25751 plasmodium
42	95.5	5.5	1090	16	Q9CFL3	Q9cfl3 lactococcus
43	95.5	5.5	1218	5	Q8IDC8	Q8idc8 plasmodium
44	95	5.4	844	10	P92948	P92948 arabidopsis
45	94.5	5.4	658	16	O25252	O25252 helicobacte

ALIGNMENTS

RESULT 1
Q95M14
ID Q95M14 PRELIMINARY; PRT; 317 AA.
AC Q95M14;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tenomodulin.
GN TNMD.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Thoroughbred; TISSUE=Tendon;
RA Hasegawa T.;
RT "Molecular cloning and characrerization of mRNA for equine
RT tenomodulin.";
RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB059407; BAB69482.2; -.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR007084; BRICHOS.
DR InterPro; IPR000345; CytC_heme_BS.
DR Pfam; PF04089; BRICHOS; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
SQ SEQUENCE 317 AA; 37165 MW; 0B7CA9D0FE12DA86 CRC64;

Query Match 97.9%; Score 1709; DB 6; Length 317;
Best Local Similarity 97.2%; Pred. No. 3.5e-132;
Matches 308; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||| |||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGGKHFWPETPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              |||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
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Db         61 TYDMEHTFYSNGEKRKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              |||||||||||:|||||||||:|||||||  |:||||||||||||||||||||| ||||||
Db        181 VTMYWINPTLIAVSELQDFEEDGEDLHFPTNDKKGIEQNEQWVVPQVKVEKTRRARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317


RESULT 2
Q8CET4
ID   Q8CET4      PRELIMINARY;      PRT;   135 AA.
AC   Q8CET4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Tenomodulin.
GN   TNMD.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK014761; BAC25447.1; -.
DR   MGD; MGI:1929885; Tnmd.
SQ   SEQUENCE   135 AA;  16069 MW;  9ADABEA41B246200 CRC64;

  Query Match             42.5%;  Score 741;  DB 11;  Length 135;
  Best Local Similarity   94.8%;  Pred. No. 3.5e-53;
  Matches  128;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        183 MYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEE 242
              |||||||||:|||||||||:||||||| :||||||||||||||||||||| |||||||:
Db          1 MYWINPTLIAVSELQDFEEDGEDLHFPTSEKKGIDQNEQWVVPQVKVEKTRHTRQASEED 60

Qy        243 LPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRV 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRV 120

Qy        303 IMPCNWWVARMLGRV 317
              |||||||||||||||
Db        121 IMPCNWWVARMLGRV 135


RESULT 3
Q7ZY92
ID   Q7ZY92      PRELIMINARY;      PRT;   338 AA.
AC   Q7ZY92;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to chondromodulin-I precursor.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC043890; AAH43890.1; -.
DR   InterPro; IPR007084; BRICHOS.
DR   Pfam; PF04089; BRICHOS; 1.
SQ   SEQUENCE   338 AA;  37839 MW;  316F8FF99047BEAE CRC64;

  Query Match             31.2%;  Score 545;  DB 13;  Length 338;
  Best Local Similarity   35.9%;  Pred. No. 1.4e-36;
  Matches  124;  Conservative   60;  Mismatches  107;  Indels   54;  Gaps   11;

Qy          6 PENCEDC--HILNAEAPKSKKICKSLKICGLVFGILALTLIVLFW--GSKHFWPEVPKKA 61
              ||: | |       |   |      : |:|  :|  :::  |::||   |: :||    |
Db         15 PEDVEQCLPPAYTAVTVKPSSNSRLLRIGAVV--LISGALLLLFGSIGAFYFWKPNDKHV 72

Qy         62 YDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCF 121
              |:: :|   ||: ::  ||||      | |::| | || :|||||: | ||| | | :||:
Db         73 YNVHYTMSINGKVQEGSMEIDSGNNLETFKTGTGNDEAVEVHDFQIGITGIRFTGGEKCY 132

Qy        122 IKTQIKV-IPEF-SEPEEEID---ENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILE 176
              || | |  ||:  |  :| :    |:| :   | | |:||| |::|:::  || : || |
Db        133 IKAQAKAHIPDVDSVTKEGLSFELEDEIMPAKFDENSLIWVAADQPVKDSSFL-SPKIQE 191

Qy        177 ICDNVTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVP-----QVKVEK 231
              :| :: ::|: ||                :|  ::|  :  : |      :|  |:
Db        192 LCADLPIFWLRPT-----------------YPKEHQRGKRETGRKVRQAQSPFEVAAEE 233

Qy        232 TRHARQ------------ASEEELPINDYT------ENGIEFDPMLDERGYCCIYCRRG 272
                 ||             ||:| | |         | |: |:|||| :| ||| |||
Db        234 RNTRRQGNRRAQAVNETQTTSEQETPFNPENPYHLEGEGGMTFNPMLDHQGVCCIDCRRS 293

Qy        273 NRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV 317
              :|:|:|||| || |:|| ||| |  ||::|||:|||||:|| |
Db        294 YTHCQRICEPLGGYDPWPYNYQGCRSACRIVMPCSWWVARILGIV 338


RESULT 4
Q80UX1
ID   Q80UX1      PRELIMINARY;      PRT;   334 AA.
AC   Q80UX1;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Leukocyte cell derived chemotaxin 1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N-3; TISSUE=Breast tumor;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N-3; TISSUE=Breast tumor;
RA   Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC045152; AAH45152.1; -.
DR   InterPro; IPR007084; BRICHOS.
DR   Pfam; PF04089; BRICHOS; 1.
SQ   SEQUENCE   334 AA;  37225 MW;  BFAAA0B224DC9944 CRC64;

  Query Match             29.9%;  Score 521;  DB 11;  Length 334;
  Best Local Similarity   36.3%;  Pred. No. 1.3e-34;
  Matches  119;  Conservative   66;  Mismatches  119;  Indels   24;  Gaps   11;

Qy          6 PENCEDCHILNAEAFKSKKICKS------LKICGLVFGILALTLIVLFW--GSKHFWPEV 57
              ||: | |    :  |: :  :  |       ||:  :|  :::  :::||   |: :||
Db         15 PEDVEFC---SPPAYTTVTVKPSGSPTRLLKVGAVV--LISGAVLLLFGAIGAFYFWKGN 69

Qy         58 PKKAYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGL 117
                 |:: ::   ||: :   |||| |   | |: |:| :| :||:||||| ||| | |
Db         70 DNHIYNVHYSMSINGKLQDGSMEIDAVNNLETFKMGSGAEEAIEVNDFKNGITGIRFAGG 129

Qy        118 QKCFIKTQIKV-IPEF-SEPEEEIDENEE--ITTTFFEQSVIWVPAEKPIENRDFLKNSK 173
              :||:|| |:|  |||  :  :: | | |   :  : | |:|||  ::|:::  || :||
Db        130 EKCYIKAQVKARIPEVGTVTKQSISELEGKIMPANYEENSLIWVAVDQPVKDSSFL-SSK 188

Qy        174 ILEICDNVTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTR 233
              |||:| :: ::|: | :  |:|     |      |:  ::   :       |      ||
Db        189 ILELCGDLPIFWLKP--MYPKEIQRERREVVRNSAPSTTRRPHSEPRGNAGPGRLSNGTR 246

Qy        234 -HARQASEEELPINDYTE---NGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPY 289
               : :  :|   | | | :     : ||| ||  | ||| |||   :|:::|||| ||||:
Db        247 PNVQDDAEPFNPDNPYHQQEGESMTFDPRLDHEGICCIECRRSYTHCQKICEPLGGYYPW 306

Qy        290 PYCYQGGRVICRVIMPCNWWVARMLGRV 317
              || ||| |  |||:|||:|||||:|| |
Db        307 PYNYQGCRSACRVVMPCSWWVARILGMV 334


RESULT 5
Q8TAY6
ID   Q8TAY6      PRELIMINARY;      PRT;   333 AA.
AC   Q8TAY6;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Chondromodulin I.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC025659; AAH25659.1; -.
DR   InterPro; IPR007084; BRICHOS.
DR   Pfam; PF04089; BRICHOS; 1.
SQ   SEQUENCE   333 AA;  36974 MW;  40A81C68ADC65FDC CRC64;

  Query Match             29.7%;  Score 518.5;  DB 4;  Length 333;
  Best Local Similarity   35.9%;  Pred. No. 2e-34;
  Matches  118;  Conservative   65;  Mismatches  119;  Indels   27;  Gaps   12;

Qy          6 PENCEDCHILNAEAF-----KSKKICKSLKICGLVFGILALTLIVLFW--GSKHFWPEVP 58
              |:: | |    :  |:      |     : ||:  :|  :::  :::||   |: :||
Db         15 PDDVEFC---SPPAYATLTVKPSSPARLLKVGAVV--LISGAVLLLFGAIGAFYFWKGSD 69

Qy         59 KKAYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQ 118
                |:: :|   ||: :   ||||     | |: |:| :| : |:||:|| ||| | | :
Db         70 SHIYNVHYTMSINGKLQDGSMEIDAGNNLETFKMGSGAEEAIAVNDFQNGITGIRFAGGE 129

Qy        119 KCFIKTQIKV-IPEF-SEPEEEID---ENEEITTTFFEQSVIWVPAEKPIENRDFLKNSK 173
              ||:|| |:|  |||  :  :: |     | : :   : | |:|||  ::|:::  || :||
Db        130 KCYIKAQVKARIPEVGAVTKQSISSKLEGKIMPVKYEENSLIWVAVDQPVKDNSFL-SSK 188

Qy        174 ILEICDNVTMYWINPTLISVSELQDFEEEGEDLHFPANEKK---GIEQNEQWVVPQVKVE 230
              :||:| :: ::|: ||      |:|     |       |   |:   |   |      ::  |
Db        189 VLELCGDLPIFWLKPTY--PKEIQRERREVVRKIVPTTTKRPHSGPRSNPG--AGRLNNE 244

Qy        231 KTRHARQASEEELPINDYTENG--IEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP 288
                    :: |:   | | | : |  : ||| ||  | ||| |||   :|:::|||| ||||
Db        245 TRPSVQEDSQAFNPDNPYHQEGESMTFDPRLDHEGICCIECRRSYTHCQKICEPLGGYYP 304

Qy        289 YPYCYQGGRVICRVIMPCNWWVARMLGRV 317
              :|| ||| |  |||||||:|||||:|| |
Db        305 WPYNYQGCRSACRVIMPCSWWVARILGMV 333


RESULT 6
Q95LQ7
ID   Q95LQ7      PRELIMINARY;      PRT;   50 AA.
AC   Q95LQ7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Tenomodulin (Fragment).
GN   TNMD.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Thoroughbred;
RA   Hasegawa T.;
RT   "Molecular cloning of equine tenomodulin gene partial cds.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB071389; BAB64928.1; -.
DR   GO; GO:0005489; F:electron transporter activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR000345; CytC_heme_BS.
DR   PROSITE; PS00190; CYTOCHROME_C; 1.
FT   NON_TER      50      50
SQ   SEQUENCE   50 AA;  5479 MW;  B56BA16A56FB5756 CRC64;

  Query Match             15.1%;  Score 264;  DB 6;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-14;
  Matches   49;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWG 49
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWG 49


RESULT 7
Q97LJ5
ID   Q97LJ5      PRELIMINARY;      PRT;   499 AA.
AC   Q97LJ5;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Histidine kinase (HAMP, HisKA and HATPase domains).
GN   CAC0565.
OS   Clostridium acetobutylicum.
OC   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1488;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
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RX   MEDLINE=21359325; PubMed=11466286;
RA   Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA   Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA   Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA   Bennett G.N., Koonin E.V., Smith D.R.;
RT   "Genome sequence and comparative analysis of the solvent-producing
RT   bacterium Clostridium acetobutylicum.";
RL   J. Bacteriol. 183:4823-4838(2001).
DR   EMBL; AE007571; AAK78544.1; -.
DR   PIR; E96969; E96969.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0016301; F:kinase activity; IEA.
DR   GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR   GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR   InterPro; IPR003594; ATPbind_ATPase.
DR   InterPro; IPR004358; Bact_sens_pr_C.
DR   InterPro; IPR003660; HAMP.
DR   InterPro; IPR005467; His_kinase.
DR   InterPro; IPR003661; His_kinA_N.
DR   InterPro; IPR008358; Lantibiot_regn.
DR   Pfam; PF00672; HAMP; 1.
DR   Pfam; PF02518; HATPase_c; 1.
DR   Pfam; PF00512; HisKA; 1.
DR   PRINTS; PR00344; BCTRLSENSOR.
DR   PRINTS; PR01780; LANTIREGPROT.
DR   SMART; SM00304; HAMP; 1.
DR   SMART; SM00387; HATPase_c; 1.
DR   SMART; SM00388; HisKA; 1.
DR   PROSITE; PS50885; HAMP; 1.
DR   PROSITE; PS50109; HIS_KIN; 1.
KW   Kinase; Complete proteome.
SQ   SEQUENCE   499 AA;  57549 MW;  7FCA501BB004F628 CRC64;

  Query Match             6.4%;  Score 112.5;  DB 16;  Length 499;
  Best Local Similarity   22.3%;  Pred. No. 0.71;
  Matches   71;  Conservative   49;  Mismatches  103;  Indels   95;  Gaps   21;

Qy         15 LNAEAFKSKKICKSLKI-CGLVFGILALTLIVL------FWGSKHFWPEVP--------- 58
Db          9 LKLYSFSKKKVVKSIRLELVVTFGICLLAAFILGSWYTGYYNDKHMMAEVDYSSGIQRIS 68

Qy         59 ------------KKAYDMEHTFYSNGEKK--KIYMEIDPVTRTE---IFRSGNGTDETLE 101
Db         69 SDMEDLKGMLDGKNSSDEINKMIDSGAKDDIKVYL-----TDTEGKVLFKSSNAKEKKID 123

Qy        102 VHD-------FKNGYTGIYFVGLQKCFIKTQIKVIPEFSEPEEEID----ENEE---ITT 147
Db        124 IHDLIVKSEKFKREYDKATVINTVNGIIKKTISL--ESVEQYNEIDGIKIDNKNAYIIVS 181

Qy        148 TFFEQSVIWV-PAEKPIENRDFLKNSKILEICDNVTMYW------------INPTLISVS 194
Db        182 GIPKQKITYIRPGYSP-----FL--SGIIAVITFVFIFYFLTNRKMEYIESVSNGLVEIS 234

Qy        195 ELQ-DFE--EEGEDLHFPANEKKGIEQNEQWVVP--QVKVEKTRHARQASEEELPINDYT 249
Db        235 KGNLDYRIMLMGED------ELKNLADNINSMASELQKRIEKEREAEKTK------NDLI 282

Qy        250 ENGIEFD---PMLDERGY 264
Db        283 TN-VSHDLRTPLTSVKGY 299


RESULT 8
Q9U459
ID   Q9U459      PRELIMINARY;      PRT;  5458 AA.
AC   Q9U459; Q9GPG4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Erythrocyte membrane-associated giant protein antigen 332.
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FCC1/HN;
RA   Shan Z.X., Yu X.B., Li X.R., Ma C.L., Fang J.M., Lu J.H., X J.;
RT   "Molecular cloning and structure analysis of the Plasmodium falciparum
RT   erythrocyte membrane-associated giant protein Ag332 (Pf332) gene.";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF202180; AAF15293.3; -.
DR   GO; GO:0003723; F:RNA binding; IEA.
DR   InterPro; IPR006763; Ag332.
DR   InterPro; IPR001313; Pumilio/Puf.
DR   Pfam; PF04671; Ag332; 179.
SQ   SEQUENCE   5458 AA;  615269 MW;  4F6A37D92BD80172 CRC64;

  Query Match             6.2%;  Score 108;  DB 5;  Length 5458;
  Best Local Similarity   24.4%;  Pred. No. 33;
  Matches   38;  Conservative   37;  Mismatches   47;  Indels   34;  Gaps    7;

Qy        136 EEEIDENEEITTTFFEQSVI-------WVPAEKPIENRDFLKNSKILEICDNVT------ 182
Db       3003 EQDVSDNEEIVE---ERSVIEEAEENVWI--EKEVE-EEGLDNEEVIDEEDSVSEQAEEE 3056

Qy        183 MYWINPTLISVSELQDFEEEGEDLHFPANE--KKGIEQNE-------------QWVVPQV 227
Db       3057 VYINEEILKESSDVEDVKVENELMNEEVNEETQSVAENNEEDKELDNYVVEETESVTEEV 3116

Qy        228 KVEKTRHARQASEEELPINDYTENGIEFDPMLDERG 263
Db       3117 VVDEVPNSKEVQEIESIIEEIVEDGLTTDDLVGQQG 3152


RESULT 9
Q8IHN3
ID   Q8IHN3      PRELIMINARY;      PRT;  5507 AA.
AC   Q8IHN3;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Antigen 332, putative.
GN   PF11_0507.
OS   Plasmodium falciparum (isolate 3D7).
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=36329;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=3D7;
RX   MEDLINE=22255705; PubMed=12368864;
RA   Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA   Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA   Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA   Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
RA   Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA   Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA   McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA   Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA   Fraser C.M., Barrell B.;
RT   "Genome sequence of the human malaria parasite Plasmodium
RT   falciparum.";
RL   Nature 419:498-511(2002).
DR   EMBL; AE014843; AAN36076.1; -.
DR   InterPro; IPR006763; Ag332.
DR   Pfam; PF04671; Ag332; 185.
SQ   SEQUENCE   5507 AA;  621156 MW;  03B095165D1490AE CRC64;

  Query Match             6.2%;  Score 108;  DB 5;  Length 5507;
  Best Local Similarity   24.4%;  Pred. No. 33;
  Matches   38;  Conservative   37;  Mismatches   47;  Indels   34;  Gaps    7;

Qy        136 EEEIDENEEITTTFFEQSVI-------WVPAEKPIENRDFLKNSKILEICDNVT------ 182
Db       2938 EQDVSDNEEIVE---ERSVIEEAEENVWI--EKEVE-EEGLDNEEVIDEEDSVSEQAEEE 2991
```

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Qy        183 MYWINPTLISVSELQDFEEEGEDLHFPANE--KKGIEQNE------------QWVVPQV 227
              :|      |   |:::| : | | ::   || :   | ||             : |  :|
Db       2992 VYINEEILKESSDVEDVKVENELMNEEVNEETQSVAENNEEDKELDNYVVEETESVTEEV 3051

Qy        228 KVEKTRHARQASEEELPINDYTENGIEFDPMLDERG 263
              |::  :::: | | | :  |:|:  | :: ::|
Db       3052 VVDEVPNSKEVQEIESIIEEIVEDGLTTDDLVGQQG 3087


RESULT 10
Q8II21
ID   Q8II21      PRELIMINARY;      PRT;  2227 AA.
AC   Q8II21;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
GN   PF11_0354.
OS   Plasmodium falciparum (isolate 3D7).
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=36329;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=3D7;
RX   MEDLINE=22255705; PubMed=12368864;
RA   Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA   Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA   Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA   Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
RA   Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA   Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA   McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA   Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA   Fraser C.M., Barrell B.;
RT   "Genome sequence of the human malaria parasite Plasmodium
RT   falciparum.";
RL   Nature 419:498-511(2002).
DR   EMBL; AE014841; AAN35938.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   2227 AA;  262840 MW;  6D5D4BEEF643339C CRC64;

  Query Match             6.0%;  Score 105.5;  DB 5;  Length 2227;
  Best Local Similarity   18.3%;  Pred. No. 17;
  Matches   44;  Conservative   56;  Mismatches   64;  Indels   77;  Gaps   11;

Qy         69 YSNGEKKKIYME----------------IDPV--TRTE----IFRSGNGTDETLEVHDFK 106
              :|| : | :|||                | :   ||:    : |    |  ::|:|:
Db       1147 FSNMDNKNVYMEGLNIQDNVNNNNNKESCDNIKHMRTKSLNFVSRESYGEHKSLDVY--- 1203

Qy        107 NGYTGIYFVGLQKCFIKTQIKVIPEFSEPEEE------IDENEEITTTFFEQSVIWVPAE 160
                    |:|::|   |:| : :: : |       ::|::  :  |:|::
Db       1204 ----------QECYVKNN-KLINKVNDKKYEDNNNSYLNEDDNASMQFYEET-----NS 1246

Qy        161 KP--IENRDFLKNSKILEICDNVTMYWINPTLISVSELQDFEEEGED------LHFPANE 212
               |  ::  : :||     : :| : |:::      |: :: | : :|      :|   ::
Db       1247 NPYIVDQENNMKNYVNNVLYNNNSNYYVDSKNYDKSK-ENAENKSDDILNNENIHTLKDQ 1305

Qy        213 KKGIEQNEQWVVPQVKVEKTRHARQ-------------------ASEEELPINDYTENG 252
              || |: | ::: |  :|  |::::                   | |||  :| : |
Db       1306 KKKIQNNNEFISEQADIENIRNSQEEVYEKEHEPLWVINASNEEKKSYEELIYSDMSSNR 1365

Qy        253 I 253
              :
Db       1366 V 1366


RESULT 11
Q8PUI9
ID   Q8PUI9      PRELIMINARY;      PRT;   494 AA.
AC   Q8PUI9;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Transposase.
GN   MM2345.
OS   Methanosarcina mazei (Methanosarcina frisia).
OC   Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC   Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX   NCBI_TaxID=2209;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Goe1 / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX   MEDLINE=22120827; PubMed=12125824;
RA   Deppenmeier U., Johann A., Hartech T., Merkl R., Schmitz R.A.,
RA   Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C.,
RA   Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
RA   Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA   Fritz H.-J., Gottschalk G.;
RT   "The genome of Methanosarcina mazei: evidence for lateral gene
RT   transfer between Bacteria and Archaea.";
RL   J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
DR   EMBL; AE013477; AAM32041.1; -.
DR   InterPro; IPR002559; Transposase_11.
DR   Pfam; PF01609; Transposase_11; 1.
KW   Complete proteome.
SQ   SEQUENCE   494 AA;  57328 MW;  0C6514323B167A5F CRC64;

  Query Match             6.0%;  Score 104.5;  DB 17;  Length 494;
  Best Local Similarity   22.6%;  Pred. No. 3.2;
  Matches   62;  Conservative   30;  Mismatches   81;  Indels  101;  Gaps   14;

Qy         56 EVPKKAYDMEHTF--YSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIY 113
              ::|::  | :       | :||     :|     | :  | ||   :  :|:
Db       184 QIPEELVDKKKRLEKIKNAKKK-----LD----EEKLKKVNITDNDARIMKYKD------ 228

Qy        114 FVGLQKCFIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSK 173
                | :|     |: |           || |:|           | |:   |  |  :
Db       229 --GSKKPSYNCQVAV----------DEKEQII----------VAADVVNEENDLHQVEP 265

Qy        174 ILEICDNVTMYWINPTLI-------SVSELQDFEEEGEDLHFPAN----EKKGIEQNEQW 222
              |::   |   |   ||::       |   |:  :||| | : | |    ||:|
Db       266 IIQNVKNTLGY--KPTIVLADAGYFSYENLEFLQEEGIDAYIPDNYYKAEKEG------- 316

Qy        223 VVPQVKVEKTRHARQASEEELPINDYTENGIEFDPMLDERGYCCIYCRRG-----NRYCR 277
                    |||  |::             ::|   |     | ||        :|  :
Db       317 --------KTRKFRKSL-------------FKYDEEKD-----CYYCPAAFEIPFSRIQK 350

Qy        278 RVCEPLLGYYPYPYCYQ----------GGRVICR 301
              |  || | ||   || |          | | | |
Db       351 RKGEPDLRYYVCSYCSQCVLKNACTESGKRTITR 384


RESULT 12
Q8IHY0
ID   Q8IHY0      PRELIMINARY;      PRT;   938 AA.
AC   Q8IHY0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Protein phosphatase 2C.
GN   PF11_0396.
OS   Plasmodium falciparum (isolate 3D7).
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=36329;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=3D7;
RX   MEDLINE=22255705; PubMed=12368864;
RA   Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA   Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA   Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA   Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
RA   Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA   Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA   McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA   Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
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RA   Fraser C.M., Barrell B.;
RT   "Genome sequence of the human malaria parasite Plasmodium
RT   falciparum.";
RL   Nature 419:498-511(2002).
DR   EMBL; AE014842; AAN35979.1; -.
DR   GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR   GO; GO:0003824; F:catalytic activity; IEA.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR   GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR   InterPro; IPR000222; PP2C.
DR   InterPro; IPR001932; PP2C-like.
DR   Pfam; PF00481; PP2C; 3.
DR   SMART; SM00332; PP2Cc; 1.
DR   PROSITE; PS01032; PP2C; 1.
SQ   SEQUENCE   938 AA;  107250 MW;  75B1B743BA5BA432 CRC64;

  Query Match             5.9%;  Score 103.5;  DB 5;  Length 938;
  Best Local Similarity   26.2%;  Pred. No. 8.6;
  Matches   67;  Conservative   32;  Mismatches   82;  Indels   75;  Gaps   16;

Qy         33 GLVFGILALTLIVLFWGSKHFW--PEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTRTE-- 88
              | | | | ||  :   |  |:  | :|:|            :|  : ||  || |
Db        702 GRVDGNLNLTRAI---GDLHYKRDPFLPQK----------DQKISAFPEITCVTLTPED 747

Qy         89 --IFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIPEF-SEPEEEI------ 139
               :| : :|      : | |:|      ||    |:||:::   |  :|   :
Db        748 EFLFLACDG------IWDCKDGQD---VVG----FVKTRLEKFEEIPDDPNNSLDNTENS 794

Qy        140 ---------DENEEITTTFFEQSVIWVPAEKPI--ENRDFLKNSKIL--EICDNVTMYWI 186
                      |:||:: :  :|: |    |  :  | || ||  :|      ||: |
Db        795 EHMNTNNNSDQNEKLKSE--DQNNINNEQENILNTSNNDFQKNENLLNENNMDNINM--- 849

Qy        187 NPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEE---EL 243
                  |:  |  |||    :| |    :   |: : | ||     |  ||   |
Db        850 ----------QEKSETEEDLDLERDEDK---HDAPPVIERKKYEKFNKLSQICEELCDEC 896

Qy        244 PINDYTEN-GIEFDPM 258
              |:| || ||  | |
Db        897 LSNNYKENDGIGCDNM 912


RESULT 13
Q8I204
ID   Q8I204      PRELIMINARY;      PRT;  1248 AA.
AC   Q8I204;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
GN   PFD0100C.
OS   Plasmodium falciparum (isolate 3D7).
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=36329;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22255708; PubMed=12368867;
RA   Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
RA   Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
RA   Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
RA   Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA   Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
RA   Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA   Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA   Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
RA   Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA   Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,
RA   Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,
RA   Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
RA   Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA   Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA   Sulston J.E., Craig A., Newbold C., Barrell B.G;
RT   "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
RL   Nature 419:527-531(2002).
DR   EMBL; AL034557; CAD49112.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   1248 AA;  154216 MW;  A6EDA94943C71AC5 CRC64;

  Query Match             5.9%;  Score 103;  DB 5;  Length 1248;
  Best Local Similarity   22.2%;  Pred. No. 13;
  Matches   74;  Conservative   43;  Mismatches   98;  Indels  118;  Gaps   17;

Qy          7 ENCEDCHI-LNAEAF-----------KSKKICKSLKICGLVFGILALTLIVLFWGSKHF 53
              | |::  : || | |            :||  || |:             |||    ||
Db        895 EECKEEEVQLNKELFLDSCIKELIKEKESKGKCKMLE------------IVLDLKDKHV 941

Qy         54 W----PEVPKK-------AYDMEHTFYSNGEKKKIY----------------------M 79
                 |: |:          ::   |  | |  ||                        |
Db        942 LINKNLEMNKRIGKNSNNLFENIKTQVKNNENNYIYEMMLNNDMNKSGKMSENDCIFDEM 1001

Qy         80 EIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKV---------- 128
               |: : :::  | |   | |:|  : |:   :  |  :|| :: :  :
Db       1002 LINNMNKSD--RIGQKKDNTIE-DNLKSNMNKLGDVN-EKCILEMEKNISMRHWENIKKN 1057

Qy        129 IPEFSEPEEEIDENEEI-------TTTFFE--QSVIWVPAEK-------PIENRDFLKNS 172
               :  | |: |   | |        :|   |  ::  :  ||       | |  |: : |
Db       1058 CTDGKEKEKNIKNVEMIENIENIGSTGKIENIRNIDEIVEEKYKSFNVEPYEENDYEEKS 1117

Qy        173 KILEICDNVTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQ-WVVPQVKVEK 231
              |||   :  :   |:| : :        |:| |       |||   |||: |
Db       1118 KILNRSNIQSNKIISPLIDN--------EKGID------EKKSDNQNEEIWY-------- 1155

Qy        232 TRHARQASEEELPINDYTENGIEFDPMLDERGY 264
                : ||:  | || | ||: | :||  |
Db       1156 ----NGLTLEEIYKNSYTRNSIEYIPYIDEEEY 1184


RESULT 14
Q8IFN0
ID   Q8IFN0      PRELIMINARY;      PRT;  1612 AA.
AC   Q8IFN0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
GN   PFD1115C.
OS   Plasmodium falciparum (isolate 3D7).
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=36329;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hamlin N., Pain A., Berriman B., Hall N., Bowman S., Churcher C.,
RA   Harris B., Harris D., Lawson D., Quail M., Barrell B.;
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL035477; CAD49270.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   1612 AA;  190946 MW;  F00A408EB4521D07 CRC64;

  Query Match             5.8%;  Score 101.5;  DB 5;  Length 1612;
  Best Local Similarity   24.1%;  Pred. No. 25;
  Matches   42;  Conservative   35;  Mismatches   70;  Indels   27;  Gaps    5;

Qy         74 KKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIPEFS 133
              |||| :: ||:   |                 : |:    ::    | | ||   :| | ::
Db       1461 KKKINIDNDPINEIE-------------ENEKSKNNPVFKFRLSKLFI---LKYIDLYT 1503

Qy        134 EPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDNVTM-YWINPTLIS 192
                | :|:| ||        :  :  :| :|  :   | |  ::|  ::: : : ||
Db       1504 -----IVKNKEFTTDCDFLYNLMIQMDKNVEKKKSLLNKGVVENDEDINVEHHINMEDEK 1558

Qy        193 VSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPIN 246
               :| | | | ||:    ||::  |: |:    : : |:    :  : | ||||
Db       1559 NEKLNDKEGEYEDVTENLNEQEAEEEAEE----EAEEEEEEEDKFLTPEHLPIN 1608


RESULT 15
Q8ENF6
```

```
ID   Q8ENF6      PRELIMINARY;      PRT;   265 AA.
AC   Q8ENF6;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical conserved protein.
GN   OB2527.
OS   Oceanobacillus iheyensis.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX   NCBI_TaxID=182710;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HTE831 / DSM 14371 / JCM 11309;
RX   MEDLINE=22220767; PubMed=12235376;
RA   Takami H., Takaki Y., Uchiyama I.;
RT   "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT   Ridge and its unexpected adaptive capabilities to extreme
RT   environments.";
RL   Nucleic Acids Res. 30:3927-3935(2002).
DR   EMBL; AP004601; BAC14483.1; -.
DR   InterPro; IPR000437; Prok_lipoprot_S.
DR   PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   265 AA;  30509 MW;  7BC76F31E881A030 CRC64;

  Query Match             5.8%;  Score 100.5;  DB 16;  Length 265;
  Best Local Similarity   20.9%;  Pred. No. 3.1;
  Matches   62;  Conservative   37;  Mismatches   88;  Indels  109;  Gaps   13;

Qy         20 FKSKKICKS---LKICGLVFGILALTLIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKK 76
              |||||  ||   ||: |::: :|   ::   |:  :: |  :  |      ::   | |
Db          9 FKSKK--KSIFILKLVGVLYVAIACVSLITTTGTASYFSEKDQDGYVRAGVWWDGSELKF 66

Qy         77 IYMEIDPVT-------RTEIFRSGNGTDE--TLEVHDFKNG------------------- 108
                 ||:|        : ||   |     :  | |::  |||
Db         67 TEKGTDPITGCDMQTIQAEIKNIGKDMKQSTTYEIYFSKNGNPKNGEKISEKELAPLKSG 126

Qy        109 ----------YTGIYFVGLQKCFIKTQIKVI--PEFSEPEEEIDENEEITTTFFEQSVIW 156
                       | |           | :|:  |||   |:: ||             |
Db        127 KQTTLKFDVDKNGSY-----------QFRVLQHPEFKNDEKQHDE-------------W 161

Qy        157 VPAEKPIENRDFLKNSKILEICDNVTMYWINPTLISVSELQDFE-----EEGEDLHFPAN 211
                      : ||:  |                 |  : || |     |  :::    :
Db        162 -------------SKKIMIKCK-----------STQDKQDKEVEVSNENQQEVEAKND 195

Qy        212 EKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENG-----IEFDPMLDER 262
               |:   : |   :|: | | |    | |||    |:  |        | :| :||:
Db        196 SKENKTEEE---LPKDKTEDTDIEEQKSEEVSDENNQEETEEIETIPETNPEIDEK 248


Search completed: March 30, 2004, 14:32:31
Job time : 47 secs
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OM protein - protein search, using sw model

Run on: March 30, 2004, 14:32:38 ; Search time 45 Seconds
(without alignments)
1843.262 Million cell updates/sec

Title: US-10-089-600-2
Perfect score: 1745
Sequence: 1 MAKNPPENCEDCHILNAEAF.....VICRVIMPCNWWVARMLGRV 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1065169 seqs, 261661801 residues

Total number of hits satisfying chosen parameters: 1065169

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1745	100.0	317	10	US-09-946-374-322	Sequence 322, App
2	1745	100.0	317	12	US-10-147-493-524	Sequence 524, App
3	1745	100.0	317	12	US-10-145-127-524	Sequence 524, App
4	1745	100.0	317	12	US-10-160-503-524	Sequence 524, App
5	1745	100.0	317	12	US-10-143-118-524	Sequence 524, App
6	1745	100.0	317	12	US-10-144-993-524	Sequence 524, App
7	1745	100.0	317	12	US-10-158-787-524	Sequence 524, App
8	1745	100.0	317	13	US-10-006-867-116	Sequence 116, App
9	1745	100.0	317	13	US-10-063-547-116	Sequence 116, App
10	1745	100.0	317	14	US-10-028-072-524	Sequence 524, App
11	1745	100.0	317	14	US-10-063-616-116	Sequence 116, App
12	1745	100.0	317	14	US-10-121-049-524	Sequence 524, App
13	1745	100.0	317	14	US-10-123-904-524	Sequence 524, App
14	1745	100.0	317	14	US-10-140-470-524	Sequence 524, App
15	1745	100.0	317	14	US-10-063-502-116	Sequence 116, App
16	1745	100.0	317	14	US-10-175-746-524	Sequence 524, App
17	1745	100.0	317	14	US-10-176-918-524	Sequence 524, App
18	1745	100.0	317	14	US-10-176-921-524	Sequence 524, App
19	1745	100.0	317	14	US-10-137-865-524	Sequence 524, App
20	1745	100.0	317	14	US-10-140-474-524	Sequence 524, App
21	1745	100.0	317	14	US-10-142-431-524	Sequence 524, App
22	1745	100.0	317	14	US-10-143-114-524	Sequence 524, App
23	1745	100.0	317	14	US-10-140-002-524	Sequence 524, App
24	1745	100.0	317	14	US-10-006-856A-322	Sequence 322, App
25	1745	100.0	317	14	US-10-142-419-524	Sequence 524, App
26	1745	100.0	317	14	US-10-063-518-116	Sequence 116, App
27	1745	100.0	317	14	US-10-123-262-524	Sequence 524, App
28	1745	100.0	317	14	US-10-142-423-524	Sequence 524, App
29	1745	100.0	317	14	US-10-063-598-116	Sequence 116, App
30	1745	100.0	317	14	US-10-227-693-116	Sequence 116, App
31	1745	100.0	317	14	US-10-006-818A-322	Sequence 322, App
32	1745	100.0	317	14	US-10-121-050-524	Sequence 524, App
33	1745	100.0	317	14	US-10-141-755-524	Sequence 524, App
34	1745	100.0	317	14	US-10-143-032-524	Sequence 524, App
35	1745	100.0	317	14	US-10-123-108-524	Sequence 524, App
36	1745	100.0	317	14	US-10-123-236-524	Sequence 524, App
37	1745	100.0	317	14	US-10-123-261-524	Sequence 524, App
38	1745	100.0	317	14	US-10-140-921-524	Sequence 524, App
39	1745	100.0	317	14	US-10-140-928-524	Sequence 524, App
40	1745	100.0	317	14	US-10-015-393A-322	Sequence 322, App
41	1745	100.0	317	14	US-10-063-567-116	Sequence 116, App
42	1745	100.0	317	14	US-10-015-869A-322	Sequence 322, App
43	1745	100.0	317	14	US-10-063-538-116	Sequence 116, App
44	1745	100.0	317	14	US-10-121-045-524	Sequence 524, App
45	1745	100.0	317	14	US-10-123-292-524	Sequence 524, App

ALIGNMENTS

RESULT 1
US-09-946-374-322
; Sequence 322, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750

; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
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; PRIOR APPLICATION NUMBER: 60/099812
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; PRIOR APPLICATION NUMBER: 60/102330
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; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
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; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
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; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
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; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
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; PRIOR APPLICATION NUMBER: 60/103328
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; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
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; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257

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;  PRIOR FILING DATE: 1998-10-14
;  PRIOR APPLICATION NUMBER: 60/104987
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105000
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105002
;  PRIOR FILING DATE: 1998-10-20
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;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/105169
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105266
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105693
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105694
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105807

  Query Match             100.0%;  Score 1745;  DB 10;  Length 317;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-156;
  Matches  317;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317


RESULT 2
US-10-147-493-524
; Sequence 524, Application US/10147493
; Publication No. US20040029217A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C345
;  CURRENT APPLICATION NUMBER: US/10/147,493
;  CURRENT FILING DATE:  2002-05-17
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 524
;   LENGTH: 317
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-147-493-524

  Query Match             100.0%;  Score 1745;  DB 12;  Length 317;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-156;
  Matches  317;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317


RESULT 3
US-10-145-127-524
; Sequence 524, Application US/10145127
; Publication No. US20040033558A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C252
;  CURRENT APPLICATION NUMBER: US/10/145,127
;  CURRENT FILING DATE:  2002-05-13
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 524
;   LENGTH: 317
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-145-127-524
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  Query Match           100.0%;  Score 1745;  DB 12;  Length 317;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-156;
  Matches  317;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317


RESULT 4
US-10-160-503-524
; Sequence 524, Application US/10160503
; Publication No. US20040033559A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C446
;  CURRENT APPLICATION NUMBER: US/10/160,503
;  CURRENT FILING DATE:  2002-05-30
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 524
;   LENGTH: 317
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-160-503-524

  Query Match           100.0%;  Score 1745;  DB 12;  Length 317;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-156;
  Matches  317;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317


RESULT 5
US-10-143-118-524
; Sequence 524, Application US/10143118
; Publication No. US20040038335A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C228
;  CURRENT APPLICATION NUMBER: US/10/143,118
;  CURRENT FILING DATE:  2002-05-09
;  Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 524
;   LENGTH: 317
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-143-118-524

  Query Match           100.0%;  Score 1745;  DB 12;  Length 317;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-156;
  Matches  317;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317
```

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Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317


RESULT 6
US-10-144-993-524
; Sequence 524, Application US/10144993
; Publication No. US20040038336A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C261
;  CURRENT APPLICATION NUMBER: US/10/144,993
;  CURRENT FILING DATE:  2002-05-13
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 524
;   LENGTH: 317
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-144-993-524

  Query Match            100.0%;  Score 1745;  DB 12;  Length 317;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-156;
  Matches  317;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317


RESULT 7
US-10-158-787-524
; Sequence 524, Application US/10158787
; Publication No. US20040039164A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C449
;  CURRENT APPLICATION NUMBER: US/10/158,787
;  CURRENT FILING DATE:  2003-04-03
;  PRIOR APPLICATION NUMBER: 60/049911
;  PRIOR FILING DATE: 1997-06-18
;  PRIOR APPLICATION NUMBER: 60/056974
;  PRIOR FILING DATE: 1997-08-26
;  PRIOR APPLICATION NUMBER: 60/059113
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059115
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059117
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059122
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059184
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059352
;  PRIOR FILING DATE: 1997-09-19
;  PRIOR APPLICATION NUMBER: 60/059588
;  PRIOR FILING DATE: 1997-09-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 524
;   LENGTH: 317
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-158-787-524

  Query Match            100.0%;  Score 1745;  DB 12;  Length 317;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-156;
  Matches  317;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
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Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317
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RESULT 8
US-10-006-867-116
; Sequence 116, Application US/10006867
; Publication No. US20020119130A1
; GENERAL INFORMATION:
; APPLICANT: Eaton,Dan L.
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,Christopher J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/006,867
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/063435
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/064215
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088740
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088811
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088825
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088863
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090688
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091628
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/096012
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096757
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/096949
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/096959
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/097954
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/097971
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/097979
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106030
; PRIOR FILING DATE: 1998-10-28

; PRIOR APPLICATION NUMBER: 60/106464
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106856
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/108807
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/112419
; PRIOR FILING DATE: 1998-12-15
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; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/112853
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/113011
; PRIOR FILING DATE: 1998-12-16
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; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113408
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114223
; PRIOR FILING DATE: 1998-12-30
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; PRIOR FILING DATE: 1999-01-12
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; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 60/116843
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/119285
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/119287
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/119525
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/119549
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/120014
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/129122
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/129674
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/138387
; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: 60/144791
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/175481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/191007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/199397
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/380139
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 09/311832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380142

Query Match 100.0%; Score 1745; DB 13; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.5e-156;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317
```

RESULT 9
US-10-063-547-116
; Sequence 116, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:
; APPLICANT: Eaton,Dan L.
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,Christopher J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,547
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 116
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-547-116

Query Match 100.0%; Score 1745; DB 13; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.5e-156;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
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```
Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317


RESULT 10
US-10-028-072-524
; Sequence 524, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang
;  TITLE OF INVENTION:
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/028,072
;  CURRENT FILING DATE:  2001-12-19
;  PRIOR APPLICATION NUMBER: 60/049911
;  PRIOR FILING DATE: 1997-06-18
;  PRIOR APPLICATION NUMBER: 60/056974
;  PRIOR FILING DATE: 1997-08-26
;  PRIOR APPLICATION NUMBER: 60/059113
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059115
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059117
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059122
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059184
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059352
;  PRIOR FILING DATE: 1997-09-19
;  PRIOR APPLICATION NUMBER: 60/059588
;  PRIOR FILING DATE: 1997-09-19
;  PRIOR APPLICATION NUMBER: 60/059836
;  PRIOR FILING DATE: 1997-09-24
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/062285
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/062287
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/062814
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/062816
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063045
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063082
;  PRIOR FILING DATE: 1997-10-31
;  PRIOR APPLICATION NUMBER: 60/063127
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063327
;  PRIOR FILING DATE: 1997-10-27
;  PRIOR APPLICATION NUMBER: 60/063329
;  PRIOR FILING DATE: 1997-10-27
;  PRIOR APPLICATION NUMBER: 60/063550
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063561
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063704
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: 60/063733
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: 60/063735
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: 60/063738
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: 60/063755
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/064248
;  PRIOR FILING DATE: 1997-11-03
;  PRIOR APPLICATION NUMBER: 60/064809
;  PRIOR FILING DATE: 1997-11-07
;  PRIOR APPLICATION NUMBER: 60/065186
;  PRIOR FILING DATE: 1997-11-12
;  PRIOR APPLICATION NUMBER: 60/065846
;  PRIOR FILING DATE: 1997-11-17
;  PRIOR APPLICATION NUMBER: 60/066364
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: 60/066453
;  PRIOR FILING DATE: 1997-11-24
;  PRIOR APPLICATION NUMBER: 60/066511
;  PRIOR FILING DATE: 1997-11-24
;  PRIOR APPLICATION NUMBER: 60/066770
;  PRIOR FILING DATE: 1997-11-24
;  PRIOR APPLICATION NUMBER: 60/069212
;  PRIOR FILING DATE: 1997-12-11
;  PRIOR APPLICATION NUMBER: 60/069278
;  PRIOR FILING DATE: 1997-12-11
;  PRIOR APPLICATION NUMBER: 60/069334
;  PRIOR FILING DATE: 1997-12-11
;  PRIOR APPLICATION NUMBER: 60/069694
;  PRIOR FILING DATE: 1997-12-16
;  PRIOR APPLICATION NUMBER: 60/072320
;  PRIOR FILING DATE: 1998-01-23
;  PRIOR APPLICATION NUMBER: 60/073612
;  PRIOR FILING DATE: 1998-02-04
;  PRIOR APPLICATION NUMBER: 60/074086
;  PRIOR FILING DATE: 1998-02-09
;  PRIOR APPLICATION NUMBER: 60/074092
;  PRIOR FILING DATE: 1998-02-09
;  PRIOR APPLICATION NUMBER: 60/077791
;  PRIOR FILING DATE: 1998-03-12
;  PRIOR APPLICATION NUMBER: 60/078910
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/079294
;  PRIOR FILING DATE: 1998-03-25
;  PRIOR APPLICATION NUMBER: 60/079663
;  PRIOR FILING DATE: 1998-02-27
;  PRIOR APPLICATION NUMBER: 60/079728
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: 60/080165
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: 60/081203
;  PRIOR FILING DATE: 1998-04-09
;  PRIOR APPLICATION NUMBER: 60/081229
;  PRIOR FILING DATE: 1998-04-09
;  PRIOR APPLICATION NUMBER: 60/081695
;  PRIOR FILING DATE: 1998-04-14
;  PRIOR APPLICATION NUMBER: 60/081817
;  PRIOR FILING DATE: 1998-04-15
;  PRIOR APPLICATION NUMBER: 60/081818
;  PRIOR FILING DATE: 1998-04-15
;  PRIOR APPLICATION NUMBER: 60/082999
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;  PRIOR FILING DATE: 1998-04-24
;  PRIOR APPLICATION NUMBER: 60/083322
;  PRIOR FILING DATE: 1998-04-28
;  PRIOR APPLICATION NUMBER: 60/083545
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/084600
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/084627
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/084637
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/085149
;  PRIOR FILING DATE: 1998-05-12
;  PRIOR APPLICATION NUMBER: 60/085323
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: 60/085338
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: 60/085339
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: 60/085579
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085697
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085704
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/086414
;  PRIOR FILING DATE: 1998-05-22
;  PRIOR APPLICATION NUMBER: 60/086430
;  PRIOR FILING DATE: 1998-05-22
;  PRIOR APPLICATION NUMBER: 60/087106
;  PRIOR FILING DATE: 1998-05-28
;  PRIOR APPLICATION NUMBER: 60/088026
;  PRIOR FILING DATE: 1998-06-04
;  PRIOR APPLICATION NUMBER: 60/088730
;  PRIOR FILING DATE: 1998-06-10
;  PRIOR APPLICATION NUMBER: 60/088741
;  PRIOR FILING DATE: 1998-06-10
;  PRIOR APPLICATION NUMBER: 60/088810
;  PRIOR FILING DATE: 1998-06-10
;  PRIOR APPLICATION NUMBER: 60/088858
;  PRIOR FILING DATE: 19/98-06-11
;  PRIOR APPLICATION NUMBER: 60/089532
;  PRIOR FILING DATE: 1998-06-17
;  PRIOR APPLICATION NUMBER: 60/089599
;  PRIOR FILING DATE: 1998-06-17
;  PRIOR APPLICATION NUMBER: 60/089907
;  PRIOR FILING DATE: 1998-06-18
;  PRIOR APPLICATION NUMBER: 60/089947
;  PRIOR FILING DATE: 1998-06-19
;  PRIOR APPLICATION NUMBER: 60/090349
;  PRIOR FILING DATE: 1998-06-23
;  PRIOR APPLICATION NUMBER: 60/090429
;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: 60/090445
;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: 60/090538
;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: 60/090863
;  PRIOR FILING DATE: 1998-06-26
;  PRIOR APPLICATION NUMBER: 60/091360
;  PRIOR FILING DATE: 1998-07-01
;  PRIOR APPLICATION NUMBER: 60/091519
;  PRIOR FILING DATE: 1998-07-02
;  PRIOR APPLICATION NUMBER: 60/091982
;  PRIOR FILING DATE: 1998-07-07

  Query Match           100.0%;  Score 1745;  DB 14;  Length 317;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-156;
  Matches  317;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317


RESULT 11
US-10-063-616-116
; Sequence 116, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,616
;  CURRENT FILING DATE:  2002-05-03
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 116
;   LENGTH: 317
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-063-616-116

  Query Match           100.0%;  Score 1745;  DB 14;  Length 317;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-156;
  Matches  317;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
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```
Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317
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RESULT 12
US-10-121-049-524
; Sequence 524, Application US/10121049
; Publication No. US20030022239A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 524
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-524

Query Match 100.0%; Score 1745; DB 14; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.5e-156;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317
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RESULT 13
US-10-123-904-524
; Sequence 524, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 524
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-524

Query Match 100.0%; Score 1745; DB 14; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.5e-156;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317
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RESULT 14
US-10-140-470-524
; Sequence 524, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey

```
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C160
;  CURRENT APPLICATION NUMBER: US/10/140,470
;  CURRENT FILING DATE:  2002-05-06
;  Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 524
;   LENGTH: 317
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-140-470-524

  Query Match            100.0%;  Score 1745;  DB 14;  Length 317;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-156;
  Matches  317;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317


RESULT 15
US-10-063-502-116
; Sequence 116, Application US/10063502
; Publication No. US20030023042A1
; GENERAL INFORMATION:
;  APPLICANT: Baton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,502
;  CURRENT FILING DATE:  2002-05-01
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 116
;   LENGTH: 317
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-063-502-116

  Query Match            100.0%;  Score 1745;  DB 14;  Length 317;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-156;
  Matches  317;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKK 60

Qy         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKC 120

Qy        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIKTQIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDN 180

Qy        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTMYWINPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE 240

Qy        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVIC 300

Qy        301 RVIMPCNWWVARMLGRV 317
              |||||||||||||||||
Db        301 RVIMPCNWWVARMLGRV 317


Search completed: March 30, 2004, 14:38:19
Job time : 46 secs
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